

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 13, 2005, 09:25:40 ; Search time 94.5296 Seconds  
(without alignments)  
878.681 Million cell updates/sec

Title: US-09-819-371-6  
Perfect score: 215  
Sequence: 1 IAVEYDDTQFLRFSDDAAI.....QRDGEQTQTELVTETRPAG 215

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1726220 seqs, 386332138 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 1726220

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database : Published Applications AA:\*
- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
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  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
  - 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
  - 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
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  - 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
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  - 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
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  - 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
  - 18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
  - 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
  - 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
  - 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
  - 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	215	100.0	215	11	US-09-819-371-6
2	119	55.3	271	9	US-09-925-301-1431
3	119	55.3	274	11	US-09-819-371-5
4	119	55.3	362	15	US-10-257-021-82
5	119	55.3	442	16	US-10-408-765A-1887
6	95	44.2	362	11	US-09-819-371-4
7	55	25.6	96	14	US-10-029-386-30718
8	52	24.2	186	15	US-10-264-049-4063
9	32	14.9	91	9	US-09-864-761-35461
10	32	14.9	110	9	US-09-796-692-799
11	32	14.9	110	9	US-09-796-692-2139
					Sequence 6, Appli
					Sequence 1431, Ap
					Sequence 5, Appli
					Sequence 82, Appli
					Sequence 1887, Ap
					Sequence 4, Appli
					Sequence 30718, A
					Sequence 4063, Ap
					Sequence 35461, A
					Sequence 799, App
					Sequence 2139, Ap

12	14.9	110	14	US-10-040-862-799	Sequence 799, App
13	14.9	110	14	US-10-040-862-2139	Sequence 2139, Ap
14	14.9	110	15	US-10-057-475B-799	Sequence 799, App
15	14.9	110	15	US-10-057-475B-2139	Sequence 2139, Ap
16	14.9	110	15	US-10-154-884B-799	Sequence 799, App
17	14.9	110	15	US-10-154-884B-2139	Sequence 2139, Ap
18	14.9	110	16	US-10-764-324-799	Sequence 799, App
19	14.9	110	16	US-10-764-324-2139	Sequence 2139, Ap
20	14.9	110	16	US-10-262-839-48	Sequence 48, Appli
21	14.9	198	15	US-10-264-049-3505	Sequence 3505, Ap
22	14.9	365	17	US-10-741-600-941	Sequence 941, App
23	14.0	104	9	US-09-925-302-835	Sequence 835, App
24	14.0	104	10	US-09-925-302-835	Sequence 835, App
25	14.0	371	15	US-10-085-198-72	Sequence 72, Appli
26	14.0	371	15	US-10-210-172-156	Sequence 156, App
27	13.0	91	14	US-10-029-386-31089	Sequence 31089, A
28	13.0	476	16	US-10-430-984-16	Sequence 16, Appli
29	13.0	500	16	US-10-430-984-15	Sequence 15, Appli
30	10.7	77	14	US-10-029-386-34273	Sequence 34273, A
31	10.7	96	14	US-10-029-386-28377	Sequence 28377, A
32	8.8	136	16	US-10-425-115-363890	Sequence 363890,
33	7.9	184	9	US-09-858-580-21	Sequence 21, Appli
34	7.9	184	10	US-09-847-172-21	Sequence 21, Appli
35	7.9	184	17	US-10-941-152-21	Sequence 21, Appli
36	7.9	421	15	US-10-138-588-32	Sequence 32, Appli
37	7.9	421	15	US-10-210-172-174	Sequence 174, App
38	7.4	91	9	US-09-864-761-38005	Sequence 38005, A
39	7.4	92	15	US-10-380-880-5	Sequence 5, Appli
40	7.4	145	9	US-09-810-560-8	Sequence 8, Appli
41	7.4	198	16	US-10-741-601-387	Sequence 387, App
42	7.4	198	17	US-10-741-601-1143	Sequence 1143, Ap
43	7.4	234	15	US-10-380-880-8	Sequence 8, Appli
44	7.4	251	16	US-10-741-601-384	Sequence 384, App
45	7.4	251	17	US-10-741-600-1142	Sequence 1142, Ap

ALIGNMENTS

RESULT 1  
US-09-819-371-6  
; Sequence 6, Application US/09819371  
; Publication No. US20040053344A1  
; GENERAL INFORMATION:  
; APPLICANT: Egawa, Kohji  
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Ca  
; FILE OF INVENTION: Using Thereof  
; FILE REFERENCE: 30815  
; CURRENT APPLICATION NUMBER: US/09/819,371  
; CURRENT FILING DATE: 2002-03-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 6  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-819-371-6

Query Match 100.0%; Score 215; DB 11; Length 215;  
Best Local Similarity 100.0%; Pred. No. 6.4e-203;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 IAVEYDDTQFLRFSDDAAI PRMEPREPWVEGEGPOYWEWTTGYAKANAQTDRVALRNL 60  
Db 1 IAVEYDDTQFLRFSDDAAI PRMEPREPWVEGEGPOYWEWTTGYAKANAQTDRVALRNL 60  
  
QY 61 RRYNQEAGSHTLQGNQMGDCMGPDKLLRGYHQHAWGDKYISLNEDLSRWTAAADTVAQI 120  
Db 61 RRYNQEAGSHTLQGNQMGDCMGPDKLLRGYHQHAWGDKYISLNEDLSRWTAAADTVAQI 120  
  
QY 121 TORFYEAEYAEFEPTYLEGECLELLRRYLENGKETLQRPAPKVAHHPIPSDHEATLR 180  
Db 121 TORFYEAEYAEFEPTYLEGECLELLRRYLENGKETLQRPAPKVAHHPIPSDHEATLR 180

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; Sequence 1431, Application US/09925301			
; Patent No. US20020052308A1			
; GENERAL INFORMATION:			
; APPLICANT: Rosen et al.			
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies			
; FILE REFERENCE: PAI06			
; CURRENT APPLICATION NUMBER: US/09/925,301			
; CURRENT FILING DATE: 2001-08-10			
; PRIOR APPLICATION NUMBER: PCT/US00/05882			
; PRIOR FILING DATE: 2000-03-08			
; PRIOR APPLICATION NUMBER: 60/124,270			
; PRIOR FILING DATE: 1999-03-12			
; NUMBER OF SEQ ID NOS: 1694			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 1431			
; LENGTH: 271			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-09-925-301-1431			
Query Match 55.3%; Score 119; DB 9; Length 271;			
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Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Qy	157	LQRADPPKAVAHHPISDHEATLRCWALGFYPABEITLTWQDGEEOQDTDELVETRPAG	215
Db	206	LQRADPPKAVAHHPISDHEATLRCWALGFYPABEITLTWQDGEEOQDTDELVETRPAG	264
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US-09-819-371-5			
; Sequence 5, Application US/09819371			
; Publication No. US20040053344A1			
; GENERAL INFORMATION:			
; APPLICANT: Egawa, Kohji			
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Car			
; TITLE OF INVENTION: Using Thereof			
; FILE REFERENCE: 30815			
; CURRENT APPLICATION NUMBER: US/09/819,371			
; CURRENT FILING DATE: 2002-03-15			
; NUMBER OF SEQ ID NOS: 6			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 5			
; LENGTH: 274			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
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Best Local Similarity 100.0%; Pred. No. 2e-108;			
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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## RESULT 6

US-09-819-371-4

; Sequence 4, Application US/09819371

; Publication No. US20040053344A1

; GENERAL INFORMATION:

; APPLICANT: Egawa, Kohji

; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can

; FILE REFERENCE: 30815

; CURRENT APPLICATION NUMBER: US/09/819,371

; CURRENT FILING DATE: 2002-03-15

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4

; LENGTH: 362

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-819-371-4

Query Match

Best Local Similarity 44.2%; Score 95; DB 11; Length 362;

Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 44

IAVEYVDVTQFLRDSDAALPRMPREPWEQEGPQYWEWTTGYAKANAQTDRLVALRNLL 103

Qy 61

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Db 104

RRYNQSEAGSHTLQMGNGCDMPDGRLLRGYHQA 138

## RESULT 7

US-10-029-386-30718

; Sequence 30718, Application US/10029386

; Publication No. US20030194704A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G

; FILE REFERENCE: AEOMICA-X-2

; CURRENT APPLICATION NUMBER: US/10/029,386

; CURRENT FILING DATE: 2001-12-20

; NUMBER OF SEQ ID NOS: 34288

; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1

; SEQ ID NO 30718

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO CHR6.1

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6

; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12

; OTHER INFORMATION: SWISSPROT HIT: P30511, EVALUE 2.00e-52

US-10-029-386-30718

Query Match

Best Local Similarity 25.6%; Score 55; DB 14; Length 96;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2

DPKAVHHPISDHEATLRCWALGFYPAITLTWQRDGEQTDTELVTETPAG 56

## RESULT 8

US-10-264-049-4063

; Sequence 4063, Application US/10264049

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Best Local Similarity 24.2%; Score 52; DB 15; Length 186;

Matches 100.0%; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-10-264-049-4063

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Matches 100.0%; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YAKANAQTDVRLNLLRRYNSAGSHYTLQMGNGCDMGPDGRLLRGVHQA 52

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US-09-864-761-35461
; Sequence 35461, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35461
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000507.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 24
; OTHER INFORMATION: EXPRESSED IN HL100, SIGNAL = 53
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 47
; OTHER INFORMATION: EXPRESSED IN HEAT, SIGNAL = 17
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 32
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 58
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 15
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; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 11
; OTHER INFORMATION: EST HUMAN HIT: AW820291.1, EVALUE 3.00e-52
; OTHER INFORMATION: SWISSPROT HIT: P30487, EVALUE 3.00e-53
US-09-864-761-35461

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Best Local Similarity 100.0%; Pred. No. 2.7e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 8 HHPISDHEATLRCWALGFYPAEITLTWORDGE 39

RESULT 10
US-09-796-692-799
; Sequence 799, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 799
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-796-692-799

Query Match 14.9%; Score 32; DB 9; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.2e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWORDGE 200
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Db 67 HHPISDHEATLRCWALGFYPAEITLTWORDGE 98

RESULT 11
US-09-796-692-2139
; Sequence 2139, Application US/09796692
; Publication No. US20020198362A1
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; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/09/796,692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
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; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
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; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2139
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-2139

Query Match      14.9%; Score 32; DB 9; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.2e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db

RESULT 12
US-10-040-862-799
; Sequence 799, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
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; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2139
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-692-2139

Query Match      14.9%; Score 32; DB 9; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.2e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      169 HHPISDHEATLRCWALGFYPAEITLTWQDGE 200
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        67 HHPISDHEATLRCWALGFYPAEITLTWQDGE 98

Db

RESULT 13
US-10-040-862-2139
; Sequence 2139, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2139
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-799

Query Match      14.9%; Score 32; DB 14; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.2e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      169 HHPISDHEATLRCWALGFYPAEITLTWQDGE 200
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        67 HHPISDHEATLRCWALGFYPAEITLTWQDGE 98

Db
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;/ PRIOR FILING DATE: 2000-08-07  
;/ PRIOR APPLICATION NUMBER: US 09/796,692  
;/ PRIOR FILING DATE: 2001-03-01  
;/ NUMBER OF SEQ ID NOS: 10467  
;/ SOFTWARE: FastSeq for Windows Version 3.0  
;/ SEQ ID NO 2139  
;/ LENGTH: 110  
;/ TYPE: PRT  
;/ ORGANISM: Homo sapiens  
US-10-040-862-2139

Query Match 14.9%; Score 32; DB 14; Length 110;  
Best Local Similarity 100.0%; Pred. No. 3.2e-23;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWORDGE 200  
DB 67 HHPISDHEATLRCWALGFYPAEITLTWORDGE 98

RESULT 14  
US-10-057-475B-799  
;/ Sequence 799, Application US/10057475B  
;/ Publication No. US20040002068A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Gaiger, Alexander  
;/ APPLICANT: Algate, Paul A.  
;/ APPLICANT: Mannion, Jane  
;/ APPLICANT: Clapper, Jonathan David  
;/ APPLICANT: Wang, Aijun  
;/ APPLICANT: Ordenez, Nadia  
;/ APPLICANT: Carter, Lauren  
;/ APPLICANT: McNeill, Patricia Dianne  
;/ APPLICANT: Corixa Corporation  
;/ TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
;/ FILE REFERENCE: 014058-014402US  
;/ CURRENT APPLICATION NUMBER: US/10/057,475B  
;/ CURRENT FILING DATE: 2002-01-22  
;/ PRIOR APPLICATION NUMBER: US 60/186,126  
;/ PRIOR FILING DATE: 2000-03-01  
;/ PRIOR APPLICATION NUMBER: US 60/190,479  
;/ PRIOR FILING DATE: 2000-03-17  
;/ PRIOR APPLICATION NUMBER: US 60/200,545  
;/ PRIOR FILING DATE: 2000-04-27  
;/ PRIOR APPLICATION NUMBER: US 60/200,303  
;/ PRIOR FILING DATE: 2000-04-28  
;/ PRIOR APPLICATION NUMBER: US 60/200,779  
;/ PRIOR FILING DATE: 2000-04-28  
;/ PRIOR APPLICATION NUMBER: US 60/200,999  
;/ PRIOR FILING DATE: 2000-05-01  
;/ PRIOR APPLICATION NUMBER: US 60/202,084  
;/ PRIOR FILING DATE: 2000-05-04  
;/ PRIOR APPLICATION NUMBER: US 60/206,201  
;/ PRIOR FILING DATE: 2000-05-22  
;/ PRIOR APPLICATION NUMBER: US 60/218,950  
;/ PRIOR FILING DATE: 2000-07-14  
;/ PRIOR APPLICATION NUMBER: US 60/222,903  
;/ PRIOR FILING DATE: 2000-08-03  
;/ Remaining Prior Application data removed - See File Wrapper or PALM.  
;/ NUMBER OF SEQ ID NOS: 10979  
;/ SOFTWARE: FastSeq for Windows Version 3.0  
;/ SEQ ID NO 799  
;/ LENGTH: 110  
;/ TYPE: PRT  
;/ ORGANISM: Homo sapiens  
US-10-057-475B-799

Query Match 14.9%; Score 32; DB 15; Length 110;  
Best Local Similarity 100.0%; Pred. No. 3.2e-23;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWORDGE 200

DB 67 HHPISDHEATLRCWALGFYPAEITLTWORDGE 98

RESULT 15  
US-10-057-475B-2139  
;/ Sequence 2139, Application US/10057475B  
;/ Publication No. US20040002068A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Gaiger, Alexander  
;/ APPLICANT: Algate, Paul A.  
;/ APPLICANT: Mannion, Jane  
;/ APPLICANT: Clapper, Jonathan David  
;/ APPLICANT: Wang, Aijun  
;/ APPLICANT: Ordenez, Nadia  
;/ APPLICANT: Carter, Lauren  
;/ APPLICANT: McNeill, Patricia Dianne  
;/ APPLICANT: Corixa Corporation  
;/ TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy  
;/ FILE REFERENCE: 014058-014402US  
;/ CURRENT APPLICATION NUMBER: US/10/057,475B  
;/ CURRENT FILING DATE: 2002-01-22  
;/ PRIOR APPLICATION NUMBER: US 60/186,126  
;/ PRIOR FILING DATE: 2000-03-01  
;/ PRIOR APPLICATION NUMBER: US 60/190,479  
;/ PRIOR FILING DATE: 2000-03-17  
;/ PRIOR APPLICATION NUMBER: US 60/200,545  
;/ PRIOR FILING DATE: 2000-04-27  
;/ PRIOR APPLICATION NUMBER: US 60/200,303  
;/ PRIOR FILING DATE: 2000-04-28  
;/ PRIOR APPLICATION NUMBER: US 60/200,779  
;/ PRIOR FILING DATE: 2000-04-28  
;/ PRIOR APPLICATION NUMBER: US 60/200,999  
;/ PRIOR FILING DATE: 2000-05-01  
;/ PRIOR APPLICATION NUMBER: US 60/202,084  
;/ PRIOR FILING DATE: 2000-05-04  
;/ PRIOR APPLICATION NUMBER: US 60/206,201  
;/ PRIOR FILING DATE: 2000-05-22  
;/ PRIOR APPLICATION NUMBER: US 60/218,950  
;/ PRIOR FILING DATE: 2000-07-14  
;/ PRIOR APPLICATION NUMBER: US 60/222,903  
;/ PRIOR FILING DATE: 2000-08-03  
;/ Remaining Prior Application data removed - See File Wrapper or PALM.  
;/ NUMBER OF SEQ ID NOS: 10979  
;/ SOFTWARE: FastSeq for Windows Version 3.0  
;/ SEQ ID NO 2139  
;/ LENGTH: 110  
;/ TYPE: PRT  
;/ ORGANISM: Homo sapiens  
US-10-057-475B-2139

Query Match 14.9%; Score 32; DB 15; Length 110;  
Best Local Similarity 100.0%; Pred. No. 3.2e-23;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 HHPISDHEATLRCWALGFYPAEITLTWORDGE 200  
DB 67 HHPISDHEATLRCWALGFYPAEITLTWORDGE 98

Search completed: July 13, 2005, 09:46:00  
Job time : 94.5296 secs

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OM protein - protein search, using sw model

Run on: July 13, 2005, 09:15:29 ; Search time 17.1472 Seconds  
(without alignments)  
935.984 Million cell updates/sec

Title: US-09-819-371-6  
Perfect score: 215  
Sequence: 1 IAVEYDDTQFLRFDSDAAI.....QRDGEQTQDTLVELTRPAG 215

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	119	55.3	362	4	US-09-949-016-8242 Sequence 8242, Ap
2	77	35.8	120	4	US-09-513-999C-4290 Sequence 4290, Ap
3	32	14.9	274	1	US-08-222-851-1 Sequence 1, Appl
4	28	13.0	358	4	US-09-949-016-6620 Sequence 6620, Ap
5	28	13.0	360	4	US-09-949-016-8370 Sequence 8370, Ap
6	17	7.9	184	3	US-09-153-586-21 Sequence 21, Appl
7	17	7.9	184	4	US-09-558-580-21 Sequence 21, Appl
8	16	7.4	117	2	US-08-406-057-9 Sequence 9, Appl
9	16	7.4	117	3	US-08-958-316-9 Sequence 9, Appl
10	16	7.4	145	2	US-08-406-057-8 Sequence 8, Appl
11	16	7.4	145	3	US-08-958-316-8 Sequence 8, Appl
12	16	7.4	338	4	US-09-949-016-6176 Sequence 6176, Ap
13	16	7.4	339	4	US-09-949-016-8636 Sequence 8636, Ap
14	16	7.4	361	3	US-08-652-265-22 Sequence 22, Appl
15	16	7.4	361	3	US-08-834-497A-22 Sequence 22, Appl
16	16	7.4	361	3	US-09-503-444A-22 Sequence 22, Appl
17	15	7.0	92	4	US-09-673-809-25 Sequence 25, Appl
18	15	7.0	182	1	US-08-127-954-135 Sequence 135, App
19	15	7.0	182	1	US-08-127-954-151 Sequence 151, App
20	15	7.0	274	2	US-08-484-905-105 Sequence 105, App
21	15	7.0	274	2	US-08-484-905-106 Sequence 106, App
22	15	7.0	274	2	US-08-484-905-107 Sequence 107, App
23	15	7.0	274	2	US-08-484-905-108 Sequence 108, App
24	15	7.0	274	2	US-08-481-985B-105 Sequence 105, App
25	15	7.0	274	3	US-08-481-985B-106 Sequence 106, App
26	15	7.0	274	3	US-08-481-985B-107 Sequence 107, App
27	15	7.0	274	3	US-08-481-985B-108 Sequence 108, App

28	15	7.0	274	3	US-08-370-476-105 Sequence 105, App
29	15	7.0	274	3	US-08-370-476-106 Sequence 106, App
30	15	7.0	274	3	US-08-370-476-107 Sequence 107, App
31	15	7.0	274	3	US-08-370-476-108 Sequence 108, App
32	15	7.0	341	3	US-08-890-719-38 Sequence 38, Appl
33	15	7.0	365	2	US-08-484-905-97 Sequence 97, Appl
34	15	7.0	365	2	US-08-484-905-98 Sequence 98, Appl
35	15	7.0	365	2	US-08-484-905-99 Sequence 99, Appl
36	15	7.0	365	2	US-08-484-905-100 Sequence 100, App
37	15	7.0	365	2	US-08-484-905-101 Sequence 101, App
38	15	7.0	365	2	US-08-484-905-102 Sequence 102, App
39	15	7.0	365	2	US-08-484-905-103 Sequence 103, App
40	15	7.0	365	2	US-08-484-905-104 Sequence 104, App
41	15	7.0	365	3	US-08-481-985B-97 Sequence 97, Appl
42	15	7.0	365	3	US-08-481-985B-98 Sequence 98, Appl
43	15	7.0	365	3	US-08-481-985B-99 Sequence 99, Appl
44	15	7.0	365	3	US-08-481-985B-100 Sequence 100, App
45	15	7.0	365	3	US-08-481-985B-101 Sequence 101, App

ALIGNMENTS

RESULT 1  
US-09-949-016-8242  
; Sequence 8242, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE OF INVENTION: CL001307  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: fastseq for Windows Version 4.0  
; SEQ ID NO 8242  
; LENGTH: 362  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-8242  
  
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Best Local Similarity 100.0%; Pred. No. 8.5e-111;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 97 DGKDYISNEDLRSTAAQTQITQFYAEAYAEFFRYLGECELELRRYLENGKET 156  
DB 140 DGKDYISNEDLRSTAAQTQITQFYAEAYAEFFRYLGECELELRRYLENGKET 199  
QY 157 LQRADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVELTRPAG 215  
DB 200 LQRADPPKAVHHPISDHEATLRCWALGFYPAEITLTWQDGEETQDTLVELTRPAG 258  
  
RESULT 2  
US-09-513-999C-4290  
; Sequence 4290, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J. Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C







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/ MEDIUM TYPE: Tape
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/958,316
/ FILING DATE: 27-OCT-1997
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: FR 94 03179
/ FILING DATE: 18-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: OBLON, NORMAN F
/ REGISTRATION NUMBER: 24,618
/ REFERENCE/DOCKET NUMBER: 0846-0437-0
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 413-3000
/ TELEFAX: (703) 413-2220
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 117 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-958-316-9

Query Match 7.4%; Score 16; DB 3; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.8e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 EATLRCWALGFYPAEI 191
Db 20 EATLRCWALGFYPAEI 35

RESULT 10
US-08-406-057-8
; Sequence 8, Application US/08406057
; Patent No. 5856442
; GENERAL INFORMATION:
; APPLICANT: CAROSELLA, EDGARDO D
; APPLICANT: MOREAU, PHILIPPE
; APPLICANT: GLUCKMAN, ELIANE
; APPLICANT: KIRSZENBAUM, MAREK
; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
; TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 2202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,057
; FILING DATE: 17-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94 03179
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 846-331-0
; TELECOMMUNICATION INFORMATION:
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/ TELEPHONE: (703) 413-3000
/ TELEFAX: (703) 413-2220
/ TELEX: 248855 OPAT UR
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 145 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-406-057-8

Query Match 7.4%; Score 16; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 EATLRCWALGFYPAEI 191
Db 48 EATLRCWALGFYPAEI 63

RESULT 11
US-08-958-316-8
; Sequence 8, Application US/08958316
; Patent No. 6291639
; GENERAL INFORMATION:
; APPLICANT: CAROSELLA, EDGARDO D
; APPLICANT: MOREAU, PHILIPPE
; APPLICANT: GLUCKMAN, ELIANE
; APPLICANT: KIRSZENBAUM, MAREK
; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
; TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 2202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/958,316
; FILING DATE: 27-OCT-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94 03179
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0846-0437-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 145 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-958-316-8

Query Match 7.4%; Score 16; DB 3; Length 145;
Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 176 EATLRCWALGFYPAEI 191  
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Db 48 EATLRCWALGFYPAEI 63

RESULT 12  
US-09-949-016-6176  
; Sequence 6176, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6176  
; LENGTH: 338  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6176

Query Match 7.4%; Score 16; DB 4; Length 338;  
Best Local Similarity 100.0%; Pred. No. 7.3e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 EATLRCWALGFYPAEI 191  
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Db 222 EATLRCWALGFYPAEI 237

RESULT 13  
US-09-949-016-8636  
; Sequence 8636, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8636  
; LENGTH: 339  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-8636

Query Match 7.4%; Score 16; DB 4; Length 339;  
Best Local Similarity 100.0%; Pred. No. 7.4e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 EATLRCWALGFYPAEI 191  
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Db 223 EATLRCWALGFYPAEI 238

RESULT 14  
US-08-652-265-22  
; Sequence 22, Application US/08652265  
; Patent No. 6025130  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Winston J.  
; APPLICANT: Drayna, Dennis T.  
; APPLICANT: Feder, John N.  
; APPLICANT: Gnirke, Andreas  
; APPLICANT: Ruddy, David  
; APPLICANT: Tsuchihashi, Zenta  
; APPLICANT: Wolff, Roger K.  
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/652,265  
; FILING DATE: 23-MAY-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 17957-000500  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 361 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..361  
; OTHER INFORMATION: /note= "Rabbit leukocyte antigen (RLA)"  
US-08-652-265-22

Query Match 7.4%; Score 16; DB 3; Length 361;  
Best Local Similarity 100.0%; Pred. No. 7.8e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 EATLRCWALGFYPAEI 191  
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Db 222 EATLRCWALGFYPAEI 237

RESULT 15  
US-08-834-497A-22  
; Sequence 22, Application US/08834497A  
; Patent No. 6140305  
; GENERAL INFORMATION:  
; APPLICANT: Thomas, Winston J.  
; APPLICANT: Drayna, Dennis T.  
; APPLICANT: Feder, John N.  
; APPLICANT: Gnirke, Andreas  
; APPLICANT: Ruddy, David  
; APPLICANT: Tsuchihashi, Zenta  
; APPLICANT: Wolff, Roger K.  
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS  
; NUMBER OF SEQUENCES: 76

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Pennie & Edmonds LLP  
;; STREET: 1155 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 10036-2811  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC Compatible  
;; OPERATING SYSTEM: Windows 95  
;; SOFTWARE: FastSEQ for Windows Version 2.0b  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/834,497A  
;; FILING DATE: 04-APR-1997  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/652,265  
;; FILING DATE: 23-MAY-1996  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/632,673  
;; FILING DATE: 16-APR-1996  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/630,912  
;; FILING DATE: 04-APR-1996  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Poissant, Brian M.  
;; REGISTRATION NUMBER: 28,462  
;; REFERENCE/DOCKET NUMBER: 8907-0056-999  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 650-493-4935  
;; TELEFAX: 650-493-5556  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 22:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 361 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; FEATURE:  
;; NAME/KEY: Protein  
;; LOCATION: 1..361  
;; OTHER INFORMATION: /note= "Rabbit leukocyte antigen (RLA)"  
;; US-08-834-497A-22

Query Match 7.4%; Score 16; DB 3; Length 361;  
Best Local Similarity 100.0%; Pred. No. 7.8e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 176 EATLCWALGFYPAEI 191  
Db 222 EATLCWALGFYPAEI 237

Search completed: July 13, 2005, 09:29:10  
Job time : 18.1472 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model.

Run on: July 13, 2005, 08:59:16 ; Search time 169 Seconds  
(without alignments)  
1096.880 Million cell updates/sec

Title: US-09-819-371-4  
Perfect score: 362  
Sequence: 1 MAPRSLLLLSGALALTDTW.....QAAVTDSAQSGVSLTANKV 362

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0  
Searched: 1612378 seqs, 512079187 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt 03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	261	72.1	362	1 HLA_F HUMAN	P30511 homo sapien
2	245	67.7	346	2 Q8WLP5	Q8WLP5 homo sapien
3	244	67.4	460	2 Q95HC0	Q95HC0 homo sapien
4	232	64.1	346	2 Q6DU28	Q6DU28 homo sapien
5	223	61.6	324	2 Q861E9	Q861E9 homo sapien
6	223	61.6	324	2 Q861F0	Q861F0 homo sapien
7	196	54.1	254	2 Q860R0	Q860R0 homo sapien
8	174	54.1	346	2 Q8MGQ1	Q8MGQ1 homo sapien
9	148	40.9	349	2 Q6DU20	Q6DU20 homo sapien
10	148	40.9	349	2 Q6DUW0	Q6DUW0 homo sapien
11	113	31.2	346	1 LC28 PANTR	P16215 pan troglod
12	113	31.2	346	2 Q951T2	Q951T2 pan troglod
13	113	31.2	362	2 Q7YR27	Q7YR27 pan troglod
14	87	24.0	91	2 Q9TPX7	Q9TPX7 gorilla gor
15	73	20.2	316	2 Q29958	Q29958 homo sapien
16	62	17.1	314	2 Q860F6	Q860F6 macaca neme
17	61	16.9	353	2 Q9MXS6	Q9MXS6 macaca mula
18	61	16.9	353	2 Q9MXS7	Q9MXS7 macaca mula
19	61	16.9	354	2 Q70UE5	Q70UE5 macaca mula
20	61	16.9	354	2 Q70UE6	Q70UE6 macaca mula
21	61	16.9	354	2 Q70UE7	Q70UE7 macaca mula
22	61	16.9	365	2 Q66ST5	Q66ST5 macaca mula
23	61	16.9	365	2 Q9MXS5	Q9MXS5 macaca mula
24	59	16.3	59	2 Q78094	Q78094 homo sapien
25	59	16.3	348	1 HLA_F MACMU	P33617 macaca mula
26	58	16.0	354	2 Q70S10	Q70S10 macaca mula
27	58	16.0	365	2 Q617A3	Q617A3 macaca fasc
28	55	15.2	365	2 Q617A9	Q617A9 macaca fasc
29	53	14.6	354	2 Q70SH4	Q70SH4 macaca mula
30	53	14.6	365	2 Q61796	Q61796 macaca fasc
31	50	13.8	351	2 Q70P17	Q70P17 macaca mula

32	50	13.8	351	2	Q70PM0	Q70PM0 macaca mula
33	46	12.7	355	2	Q767W6	Q767W6 aotus trivi
34	45	12.4	330	2	Q30713	Q30713 macaca mula
35	45	12.4	338	2	Q95510	Q95510 leopardus p
36	45	12.4	359	2	Q30711	Q30711 macaca mula
37	44	12.2	91	2	Q7YNY3	Q7YNY3 homo sapien
38	44	12.2	91	2	Q7YNY6	Q7YNY6 homo sapien
39	44	12.2	91	2	Q7YF25	Q7YF25 homo sapien
40	44	12.2	91	2	Q9MYH8	Q9MYH8 homo sapien
41	44	12.2	91	2	Q9MYI0	Q9MYI0 homo sapien
42	44	12.2	91	2	Q9MYI2	Q9MYI2 homo sapien
43	44	12.2	259	2	Q29645	Q29645 homo sapien
44	44	12.2	273	2	Q8HWT0	Q8HWT0 homo sapien
45	44	12.2	273	2	Q8MGZ8	Q8MGZ8 homo sapien

## ALIGNMENTS

RESULT 1  
HLAF HUMAN  
ID HLAF HUMAN STANDARD; PRT; 362 AA.  
AC P30511; Q9TP68;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DE HLA class I histocompatibility antigen, alpha chain F precursor (HLA F antigen) (Leukocyte antigen F) (CDA12).  
GN Name=HLA-F; Synonyms=HLA-5.4, HLAF;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90111605; PubMed=1688605;  
RA Geraghty D.E., Wei X., Orr H.T., Koller B.H.;  
RT "Human leukocyte antigen F (HLA-F). An expressed HLA gene composed of a class I coding sequence linked to a novel transcribed repetitive element."  
RL J. Exp. Med. 171:1-18(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91197889; PubMed=1707659;  
RA Lury D., Epstein H., Holmes N.;  
RT "The human class I MHC gene HLA-F is expressed in lymphocytes."  
RL Int. Immunol. 2:531-537(1990).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20189617; PubMed=10727083;  
RA Hampe A., Coriton O., Andrieux N., Carn G., Lepourcelet M., Mottier S., Dreano S., Gatiou M.T., Hitte C., Soriano N., Galibert F.;  
RT "A 356-Kb sequence of the subtelomeric part of the MHC class I region."  
RL DNA Seq. 10:263-299(1999).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX Shima S., Tamiya G., Oka A., Inoko H.;  
RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region."  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A., AND VARIANT PRO-272.  
RX MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;  
RA Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L., Almeida J.P., Ambrose K.D., Bailey J., Banerjee R., Barker D.J., Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P., Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.V., Burford D.C., Burrill W., Burton J., Carder C., Carter N.P., Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Cobley V., Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,

FT	VARIANT	272	272	S ->P (in dBSNP-1736924) .
FT				/FTID=VAR_018327.
SQ	SEQUENCE	362 AA;	40568 MW;	B8DD041F820A34E1 CRC64;
	Query Match		72.1%;	Score 261; DB 1; Length 362;
	Best Local Similarity		99.7%;	Pred. No. 3.3e-243;
	Matches 361; Conservative		0; Mismatches	1; Indels 0; Gaps 0;
Qy	1	MAPRSLLLLSGALALTD	TWAGSHSLRYFSTAVSR	PGRGEPRYIAVEYDDTQFLRFDSD 60
Db	1	MAPRSLLLLSGALALTD	TWAGSHSLRYFSTAVSR	PGRGEPRYIAVEYDDTQFLRFDSD 60
Qy	61	AAIPRMEPRPWEQBPQW	ETTTGAKANAQTDRLVAL	NLLRRYNQSGSHTLQGMN 120
Db	61	AAIPRMEPRPWEQBPQW	ETTTGAKANAQTDRLVAL	NLLRRYNQSGSHTLQGMN 120
Qy	121	GCDMGPDGRLLRGHQ	YHAYDGKDIYISNEDLR	SWTAADTVAQITQRFYEAEYAEERPT 180
Db	121	GCDMGPDGRLLRGHQ	YHAYDGKDIYISNEDLR	SWTAADTVAQITQRFYEAEYAEERPT 180
Qy	181	LEGECELELLRRYLENG	LETLQRADPPKAHVAHP	IPISDHEATLRCWALGFYPAEITLTWQR 240
Db	181	LEGECELELLRRYLENG	LETLQRADPPKAHVAHP	IPISDHEATLRCWALGFYPAEITLTWQR 240
Qy	241	DGSEQQTDTLQVTRP	AGDGTFOKWAADVPSGE	QRYTCHVOHEGLPOPLILRWESQP 300
Db	241	DGSEQQTDTLQVTRP	AGDGTFOKWAADVPSGE	QRYTCHVOHEGLPOPLILRWESQP 300
Qy	301	PTPIVGIVAGLVVLGA	VTGAVVAAMWKKSSDR	NRGYSQAAVTDTSAGSGVSLTAN 360
Db	301	PTPIVGIVAGLVVLGA	VTGAVVAAMWKKSSDR	NRGYSQAAVTDTSAGSGVSLTAN 360
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ID	Q8WLP5			
AC	Q8WLP5;			
DT	01-MAR-2002 (T			EMBLrel. 20, Created)
DT	01-MAR-2002 (T			EMBLrel. 20, Last sequence update)
DT	25-OCT-2004 (T			EMBLrel. 28, Last annotation update)
GN	MHC class Ib antigen (HLA-F protein).			
DE	Name=HLA-F;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.;			
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.			
RT	[2]			
RP	SEQUENCE FROM N.A.			
RA	He X., Xu L., Liu Y., Zeng Y.;			
RL	"Identification of a novel HLA-F allele - HLA-F*010102.";			
RT	[3]			
RP	SEQUENCE FROM N.A.			
RA	He X., Xu L., Liu Y., Zeng Y.;			
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.			
RT	[4]			
RP	SEQUENCE FROM N.A.			
RA	TSSUE=Lymph;			
RL	MEDLINE=22398257; PubMed=14705989;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lymph;  
 RA Strausberg R.;  
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
 RN [6]

RP SEQUENCE FROM N.A.  
 RA Pyo C.-W., Ishitani A., Moore Y.F., Geraghty D.E.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF523285; AAM74980.1; -  
 DR EMBL; AF523287; AAM74982.1; -  
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 DR EMBL; AV645742; AAT73225.1; -  
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 DR EMBL; AV645746; AAT73229.1; -  
 DR EMBL; AV645749; AAT73232.1; -  
 DR EMBL; AV645750; AAT73233.1; -  
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 DR EMBL; AV645752; AAT73235.1; -  
 DR EMBL; AV645753; AAT73236.1; -  
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 DR EMBL; AV645758; AAT73241.1; -  
 DR EMBL; AV645759; AAT73242.1; -  
 DR EMBL; AF523286; AAM74981.1; -  
 DR HSP; Q5TQH5; 1B0R.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR Pfam; PF07654; C1-set; 1.  
 DR PRINTS; PR01638; MHC\_I.1.  
 DR ProDom; PD000050; MHC\_I; 1.  
 DR SMART; SM00407; IGC1; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Transmembrane.  
 SQ SEQUENCE 346 AA; 39051 MW; D4782AA4697D57B2 CRC64;

Query Match 67.7%; Score 245; DB 2; Length 346;  
 Best Local Similarity 99.7%; Pred. No. 9.2e-228;  
 Matches 345; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPRSLLLSGALALTDTWAGSHSLRYSTAVSRGRGEPRIYAYEYVDDTQFLRFDSD 60  
 DB 1 MAPRSLLLSGALALTDTWAGSHSLRYSTAVSRGRGEPRIYAYEYVDDTQFLRFDSD 60

QY 61 AAIPIRPEPWPVEQSPQWETTTGYAKANAQTDRLVALNLLRRYNSAGSHTLQGMN 120  
 DB 61 AAIPIRPEPWPVEQSPQWETTTGYAKANAQTDRLVALNLLRRYNSAGSHTLQGMN 120  
 QY 121 GCDMGPDGRLRGYHGHVGDGKDYISLNEDLRSWTAADTVAQITQRYEAEVEAEERTY 180  
 DB 121 GCDMGPDGRLRGYHGHVGDGKDYISLNEDLRSWTAADTVAQITQRYEAEVEAEERTY 180  
 QY 181 LEGECLELRRYLENGLETLQADPPKAVHHPISDHEATLRCWALGFPYPAETTLTQWR 240  
 DB 181 LEGECLELRRYLENGLETLQADPPKAVHHPISDHEATLRCWALGFPYPAETTLTQWR 240  
 QY 241 DGEEOQTDELVELTRPAGDGTFOKAAVVPSPSEBQRYTCHVQHEGLPQLILRWEQSPQ 300  
 DB 241 DGEEOQTDELVELTRPAGDGTFOKAAVVPSPSEBQRYTCHVQHEGLPQLILRWEQSPQ 300  
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 ID Q95HCO PRELIMINARY; PRT; 460 AA.  
 AC Q95HCO;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DE HLA-F protein (Fragment).  
 GN Name=HLA-F;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA Strausberg R.;  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC009260; AAO9260.2; -  
 DR HSP; Q5TQH5; 1B0R.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG\_c1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR001039; MHC\_I.  
 Pfam; PF07654; C1-set; 1.  
 DR Pfam; PF00129; MHC\_I; 1.

DR PRINTS; PRO1638; MHCCLASSI.  
 DR ProDom; PD000050; MHC I; 1.  
 DR SMART; SM00407; IGc1; 1.  
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 DR PROSITE; PS00290; IG\_MHC; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 460 AA; 52263 MW; C1A0B6891978D93E CRC64;

Query Match 67.4%; Score 244; DB 2; Length 460;  
 Best Local Similarity 99.7%; Pred. No. 1.1e-226; Indels 0; Gaps 0;  
 Matches 344; Conservative 0; Mismatches 1;

QY 1 MAPRSLLLSGALALTDWTAGSHSLRYFSTAVSRPGRGEPRIYIAVEYVDDTQFLRFDS 60  
 DB 19 MAPRSLLLSGALALTDWTAGSHSLRYFSTAVSRPGRGEPRIYIAVEYVDDTQFLRFDS 78  
 QY 61 AAI PRMEPREPVEQEGPOYWEWTTGYAKANAQTDRLVALNLLRRYNQSEAGSHTLQGN 120  
 DB 79 AAI PRMEPREPVEQEGPOYWEWTTGYAKANAQTDRLVALNLLRRYNQSEAGSHTLQGN 138  
 QY 121 GCDMGPDGRLRGYHQHAYDGDYISLNEDLSWTAADTVAQITQRFYEAEEYAEFFRTY 180  
 DB 139 GCDMGPDGRLRGYHQHAYDGDYISLNEDLSWTAADTVAQITQRFYEAEEYAEFFRTY 198  
 QY 181 LECELELLRRYLENGLETQADPPKAHVAHPISDHEATLRCWALGFYPABEITLTWQR 240  
 DB 199 LECELELLRRYLENGLETQADPPKAHVAHPISDHEATLRCWALGFYPABEITLTWQR 258  
 QY 241 DGEQOTQDTLVEYTRPAGDGTQKAAVVPVSGEEQRYTCHVQHEGLPQPLILRWEQSPQ 300  
 DB 259 DGEQOTQDTLVEYTRPAGDGTQKAAVVPVSGEEQRYTCHVQHEGLPQPLILRWEQSPQ 318  
 QY 301 PTPIPIVIGIVAGLVIGAVVTGAVVAAMVRKSSDRNRGSYQAA 345  
 DB 319 PTPIPIVIGIVAGLVIGAVVTGAVVAAMVRKSSDRNRGSYQAA 363

## RESULT 4

Q6DU28 PRELIMINARY; PRT; 346 AA.  
 AC Q6DU28;  
 DT 25-OCT-2004 (TREMBLrel. 28, Created)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
 DE MHC class Ib antigen.  
 GN Name=HLA-F;  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Pyo C.-W., Ishitani A., Moore Y.F., Geraghty D.E.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY645747; AAT73230.1; -  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR001039; MHC I.  
 DR Pfam; PF07654; Cl-set; 1.  
 DR Pfam; PF00047; Ig; 1.  
 DR Pfam; PF00129; MHC I; 1.  
 DR PRINTS; PRO1638; MHCCLASSI.  
 DR ProDom; PD000050; MHC I; 1.  
 DR SMART; SM00407; IGc1; 1.  
 DR PROSITE; PS00835; IG LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Transmembrane.  
 SQ SEQUENCE 346 AA; 39079 MW; 8C370BFB40B15818 CRC64;

Query Match 64.1%; Score 232; DB 2; Length 346;

Best Local Similarity 99.7%; Pred. No. 3.4e-215;  
 Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 LALTDWTAGSHSLRYFSTAVSRPGRGEPRIYIAVEYVDDTQFLRFDSDAAI PRMEPREPV 73  
 DB 14 LALTDWTAGSHSLRYFSTAVSRPGRGEPRIYIAVEYVDDTQFLRFDSDAAI PRMEPREPV 73  
 QY 74 EQEGPOYWEWTTGYAKANAQTDRLVALNLLRRYNQSEAGSHTLQGNMGCDMGPDGRLRG 133  
 DB 74 EQEGPOYWEWTTGYAKANAQTDRLVALNLLRRYNQSEAGSHTLQGNMGCDMGPDGRLRG 133  
 QY 134 YHQHAYDGDYISLNEDLSWTAADTVAQITQRFYEAEEYAEFFTYLECELELLRRYL 193  
 DB 134 YHQHAYDGDYISLNEDLSWTAADTVAQITQRFYEAEEYAEFFTYLECELELLRRYL 193  
 QY 194 ENGLTQLRADPPKAHVAHPISDHEATLRCWALGFYPABEITLTWQRGEEQOTQDTLVE 253  
 DB 194 ENGLTQLRADPPKAHVAHPISDHEATLRCWALGFYPABEITLTWQRGEEQOTQDTLVE 253  
 QY 254 TRPAGDGTQKAAVVPVSGEEQRYTCHVQHEGLPQPLILRWEQSPQPTPIPIVIGIVAGLV 313  
 DB 254 TRPAGDGTQKAAVVPVSGEEQRYTCHVQHEGLPQPLILRWEQSPQPTPIPIVIGIVAGLV 313  
 QY 314 VLGA VVTGAVVAAMVRKSSDRNRGSYQAAV 346  
 DB 314 VLGA VVTGAVVAAMVRKSSDRNRGSYQAAV 346

## RESULT 5

Q861E9 PRELIMINARY; PRT; 324 AA.  
 AC Q861E9;  
 DT 01-JUN-2003 (TREMBLrel. 24, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE MHC class I antigen (Fragment).  
 GN Name=HLA-F;  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Liu Y., Xu L., Zeng Y., He X.;  
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY221102; AAC34407.1; -  
 DR HSP; Q9TQH5; 1B0R.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR001039; MHC I.  
 DR Pfam; PF07654; Cl-set; 1.  
 DR Pfam; PF00129; MHC I; 1.  
 DR PRINTS; PRO1638; MHCCLASSI.  
 DR ProDom; PD000050; MHC I; 1.  
 DR PROSITE; PS00835; IG LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 324 AA; 36518 MW; E3E028177D2716F4 CRC64;

Query Match 61.6%; Score 223; DB 2; Length 324;  
 Best Local Similarity 99.7%; Pred. No. 1.6e-206;  
 Matches 323; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 SLLLLSGALALTDWTAGSHSLRYFSTAVSRPGRGEPRIYIAVEYVDDTQFLRFDSAAIP 64  
 DB 1 SLLLLSGALALTDWTAGSHSLRYFSTAVSRPGRGEPRIYIAVEYVDDTQFLRFDSAAIP 60  
 QY 65 RWEPRVVEQEGPOYWEWTTGYAKANAQTDRLVALNLLRRYNQSEAGSHTLQGNMGCDM 124



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Db 61 RMEPRFWVEQEGQYWEWTTGYAKANAQTDVALNLLRRYNSAGSHTLQMGCDM 120
Qy 125 GPDGRLRGYHQHAYDQKDYISLNEDLSRWTAADTVAQITQRFYEAEEAEFFTYLEGE 184
Db 121 GPDGRLRGYHQHAYDQKDYISLNEDLSRWTAADTVAQITQRFYEAEEAEFFTYLEGE 180
Qy 185 CLELLRRYLENGLETQORADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQDGE 244
Db 181 CLELLRRYLENGLETQORADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQDGE 240
Qy 245 QTQDTVELVETRPAGDGTFOKAAVVPVSGEQRVTCHVQHEGLPQPLILRWESQPQTIP 304
Db 241 QTQDTVELVETRPAGDGTFOKAAVVPVSGEQRVTCHVQHEGLPQPLILRWESQPQTIP 300
Qy 305 IVGIVAGLVVLGAVVTGAVVAAM 328
Db 301 IVGIVAGLVVLGAVVTGAVVAAM 324

RESULT 6
Q861FO PRELIMINARY; PRT; 324 AA.
AC Q861FO;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Nonclassical MHC class I antigen (Fragment).
GN Name=HLA-F;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA He X., Xu L., Liu Y., Zeng Y.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY216882; AAC37689.1; -
DR HSSP; Q9TQHS; I80R.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGC1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1_1
FT NON_TER 324 324
SQ SEQUENCE 324 AA; 36518 MW; E3E028177D2716F4 CRC64;

Query Match 61.6%; Score 223; DB 2; Length 324;
Best Local Similarity 99.7%; Pred. No. 1.6e-206;
Matches 323; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 SLILLLSGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIYAVYVDQTQFLRFDSDAIP 64
Db 1 SLILLLSGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIYAVYVDQTQFLRFDSDAIP 60
Qy 65 RMEPRFWVEQEGQYWEWTTGYAKANAQTDVALNLLRRYNSAGSHTLQMGCDM 124
Db 61 RMEPRFWVEQEGQYWEWTTGYAKANAQTDVALNLLRRYNSAGSHTLQMGCDM 120
Qy 125 GPDGRLRGYHQHAYDQKDYISLNEDLSRWTAADTVAQITQRFYEAEEAEFFTYLEGE 184
Db 121 GPDGRLRGYHQHAYDQKDYISLNEDLSRWTAADTVAQITQRFYEAEEAEFFTYLEGE 180
Qy 185 CLELLRRYLENGLETQORADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQDGE 244

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Db 181 CLELLRRYLENGLETQORADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQDGE 240
Qy 245 QTQDTVELVETRPAGDGTFOKAAVVPVSGEQRVTCHVQHEGLPQPLILRWESQPQTIP 304
Db 241 QTQDTVELVETRPAGDGTFOKAAVVPVSGEQRVTCHVQHEGLPQPLILRWESQPQTIP 300
Qy 305 IVGIVAGLVVLGAVVTGAVVAAM 328
Db 301 IVGIVAGLVVLGAVVTGAVVAAM 324

RESULT 7
Q860RO PRELIMINARY; PRT; 254 AA.
AC Q860RO;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MHC class Ib antigen.
GN Name=HLA-F;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Y., He X., Xu L., Zeng Y.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY253271; AAC86775.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001039; MHC_I.
DR Pfam; PF00129; MHC_I; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
SQ SEQUENCE 254 AA; 28588 MW; C81F225D409AED2 CRC64;

Query Match 54.1%; Score 196; DB 2; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.6e-180;
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPRSLLLSGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIYAVYVDQTQFLRFDSD 60
Db 1 MAPRSLLLSGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIYAVYVDQTQFLRFDSD 60
Qy 61 AAIPRMEPRFWVEQEGQYWEWTTGYAKANAQTDVALNLLRRYNSAGSHTLQGMN 120
Db 61 AAIPRMEPRFWVEQEGQYWEWTTGYAKANAQTDVALNLLRRYNSAGSHTLQGMN 120
Qy 121 GCDMGPDGRLRGYHQHAYDQKDYISLNEDLSRWTAADTVAQITQRFYEAEEAEFFTY 180
Db 121 GCDMGPDGRLRGYHQHAYDQKDYISLNEDLSRWTAADTVAQITQRFYEAEEAEFFTY 180
Qy 181 LEGECELELLRRYLENG 196
Db 181 LEGECELELLRRYLENG 196

RESULT 8
Q8MGQ1 PRELIMINARY; PRT; 346 AA.
AC Q8MGQ1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MHC class Ib antigen.
GN Name=HLA-F;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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RA	Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.;
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
[2]	
RN	SEQUENCE FROM N.A.
RP	Pvo C.-W., Ishitani A., Moore Y.F., Geraghty D.E.;
RA	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL	EMBL; AF523284; AAU74979.1; -
DR	EMBL; AF523291; AAU74986.1; -
DR	EMBL; AF523292; AAU74987.1; -
DR	EMBL; AY645748; AAT73231.1; -
DR	EMBL; AY645754; AAT73237.1; -
DR	HSP; Q9TQHS; 1B0R.
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0006955; P:immune response; IEA.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig cl.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR001039; MHC_I.
DR	Pfam; PF07654; Cl-set; 1.
DR	Pfam; PF00129; MHC_I; 1.
DR	PRINTS; PR01638; MHCCLASSI.
DR	ProDom; PD000050; MHC_I; 1.
DR	SMART; SM00407; IGcl; 1.
DR	PROSITE; PS00835; IG_LIKE; 1.
DR	PROSITE; PS00290; IG_MHC; 1.
DR	Transmembrane.
KW	Transmembrane.
SQ	SEQUENCE 346 AA; 39061 MW; D4782968A67E9B7D CRC64;
Query Match 54.1%; Score 196; DB 2; Length 346;	
Best Local Similarity 100.0%; Pred.No. 2.le-180;	
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 MAPRSLLLLSGALALDTTWAGSHSLRYFSTAVSRPGRGEPRTAYEVYDDTQFLRFDS 60 
Dd	1 MAPRSLLLLSGALALDTTWAGSHSLRYFSTAVSRPGRGEPRTAYEVYDDTQFLRFDS 60 
Qy	61 AAPRMPEPREPWPVEGEPQYWETWTGYAKANAQTDRVALNLLRRYNSEAGSHTLOGMN 120 
Dd	61 AAPRMPEPREPWPVEGEPQYWETWTGYAKANAQTDRVALNLLRRYNSEAGSHTLOGMN 120 
Qy	121 GCDMPGPGRLLRGVHQAIDKDYISLNEDLSRWTAADTVAQITQTFYEAEYAEFPFY 180 
Dd	121 GCDMPGPGRLLRGVHQAIDKDYISLNEDLSRWTAADTVAQITQTFYEAEYAEFPFY 180 
Qy	181 LEGECLELLRRYLENG 196 
Dd	181 LEGECLELLRRYLENG 196 
RESULT 9	
Q6DU20	PRELIMINARY; PRT; 346 AA.
ID	Q6DU20 PRELIMINARY; PRT; 346 AA.
AC	Q6DU20;
DT	25-OCT-2004 (TrEMBLrel. 28, Created)
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE	MHC class Ib antigen.
GN	Name=HLA-F;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCHI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Pvo C.-W., Ishitani A., Moore Y.F., Geraghty D.E.;
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY645755; AAT73238.1; -
DR	GO; GO:0016020; C:membrane; IEA.
DR	GO; GO:0006955; P:immune response; IEA.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig cl.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR001039; MHC_I.

Query Match 40.9%; Score 148; DB 2; Length 349;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-134; Indels 0; Gaps 0;  
 Matches 148; Conservative 0; Mismatches 0;

QY 198 ETQLRADPPKAAHVAHPISDHEATLRCWALGFYPAETITLTWQRDGEQOTDELVETRPA 257  
 DB 112 ETQLRADPPKAAHVAHPISDHEATLRCWALGFYPAETITLTWQRDGEQOTDELVETRPA 171

QY 258 GDCFTQKAAVVPVSGEEQRYTCHVQHEGLPQPLILRWESQPTPIVIGIVAGLVVLGA 317  
 DB 172 GDCFTQKAAVVPVSGEEQRYTCHVQHEGLPQPLILRWESQPTPIVIGIVAGLVVLGA 231

QY 318 VVTGAVVAAVMWRKSSDRNGYSQAA 345  
 DB 232 VVTGAVVAAVMWRKSSDRNGYSQAA 259

## RESULT 11

ID 1C28\_PANTR STANDARD; PRT; 346 AA.  
 AC F16215;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-APR-1993 (Rel. 25, Last annotation update)  
 DE CH1A class I histocompatibility antigen, CH28 alpha chain precursor.  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP MEDLINE FROM N.A.  
 RX MEDLINE=90201944; PubMed=1690682;  
 RA Lawlor D.A., Warren E., Ward F.E., Parham P.;  
 RT "HLA-A and B polymorphisms predate the divergence of humans and chimpanzees.";  
 RL Nature 335:268-271(1988).  
 CC -!- FUNCTION: Involved in the presentation of foreign antigens to the immune system.  
 CC -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).  
 CC -----  
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 CC -----  
 CC EMBL; M30685; AAA87973.1; --  
 DR HSSP; Q29961; 1HSA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_C1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR001039; MHC\_I.  
 DR Pfam; PF00047; Ig; 1.  
 DR Pfam; PF00129; MHC\_I; 1.  
 DR PRINTS; PR01638; MHCCLASSI.  
 DR ProDom; PD000050; MHC\_I; 1.  
 DR SMART; SM00407; IGC1; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Glycoprotein; MHC I; Signal; Transmembrane.  
 FT SIGNAL 1 21  
 FT CHAIN 22 346 CH1A class I histocompatibility antigen, CH28 alpha chain.  
 FT DOMAIN 22 111 Extracellular alpha-1.

FT DOMAIN 112 203 Extracellular alpha-2.  
 FT DOMAIN 204 295 Extracellular alpha-3.  
 FT DOMAIN 296 305 Connecting peptide.  
 FT TRANSMEM 306 329  
 FT DOMAIN 330 346 Cytoplasmic tail.  
 FT DISULFID 122 185 By similarity.  
 FT DISULFID 224 280 By similarity.  
 FT CARBOHYD 107 107 N-linked (GlcNAc...) (By similarity).  
 SQ SEQUENCE 346 AA; 39084 MW; F838882D5C2E0971 CRC64;

Query Match 31.2%; Score 113; DB 1; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-100; Indels 0; Gaps 0;  
 Matches 113; Conservative 0; Mismatches 0;

QY 84 TTGYAKANAQTRVALRNLRLRYNQSEAGSHTLQGNMGCDMGDPGRLRGYHQAHDGKD 143  
 DB 84 TTGYAKANAQTRVALRNLRLRYNQSEAGSHTLQGNMGCDMGDPGRLRGYHQAHDGKD 143

QY 144 YISLNEDLSRWSAADTVAQITQRFYEAEEYAEFFTYLEGECLLELRLRYLENG 196  
 DB 144 YISLNEDLSRWSAADTVAQITQRFYEAEEYAEFFTYLEGECLLELRLRYLENG 196

RESULT 12

Q95IT2 PRELIMINARY; PRT; 346 AA.  
 ID Q95IT2;  
 AC Q95IT2; (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE MHC class I antigen.  
 GN Name=Patr-F;  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP MEDLINE FROM N.A.  
 RX MEDLINE=21291697; PubMed=11398964; DOI=10.1007/s002510100318;  
 RA Adams E.J., Parham P.;  
 RT "Genomic analysis of common chimpanzee major histocompatibility complex class I genes.";  
 RL Immunogenetics 53:200-208(2001).  
 DR EMBL; AF338355; AAK77479.1; --  
 DR HSSP; Q9TQH5; 1BOR.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_C1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR001039; MHC\_I.  
 DR Pfam; PF07654; C1-set; 1.  
 DR Pfam; PF00129; MHC\_I; 1.  
 DR PRINTS; PR01638; MHCCLASSI.  
 DR ProDom; PD000050; MHC\_I; 1.  
 DR SMART; SM00407; IGC1; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 1.  
 DR PROSITE; PS00290; IG\_MHC; 1.  
 KW Transmembrane.  
 SQ SEQUENCE 346 AA; 39009 MW; 0ECF12B7DB17B814 CRC64;

Query Match 31.2%; Score 113; DB 2; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-100; Indels 0; Gaps 0;  
 Matches 113; Conservative 0; Mismatches 0;

QY 84 TTGYAKANAQTRVALRNLRLRYNQSEAGSHTLQGNMGCDMGDPGRLRGYHQAHDGKD 143  
 DB 84 TTGYAKANAQTRVALRNLRLRYNQSEAGSHTLQGNMGCDMGDPGRLRGYHQAHDGKD 143

QY 144 YISLNEDLSRWSAADTVAQITQRFYEAEEYAEFFTYLEGECLLELRLRYLENG 196  
 DB 144 YISLNEDLSRWSAADTVAQITQRFYEAEEYAEFFTYLEGECLLELRLRYLENG 196

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RESULT 13
Q7YR27
ID Q7YR27 PRELIMINARY; PRT; 362 AA.
AC Q7YR27;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Class Ib.
GN Name=Patr-F;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]_TaxID=9598;
RP SEQUENCE FROM N.A.
RX MEDLINE=22709134; PubMed=12799463; DOI=10.1073/pnas.1230533100;
RA Anzai T., Shiina T., Kimura N., Yanagiya K., Kohara S., Shigenari A.,
RA Yamagata T., Kuleki J.K., Naruse T.K., Fujimori Y., Fukuzumi Y.,
RA Yamazaki M., Tashiro H., Iwamoto C., Umehara Y., Inanishi T.,
RA Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H.;
RT "Comparative sequencing of human and chimpanzee MHC class I regions
RT unveils insertions/deletions as the major path to genomic
RT divergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713 (2003).
DR EMBL; AB100087; BAC78191.1; -.
DR HSP; O9TQHS; 1B0R.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR010339; MHC_I.
DR InterPro; IPR010579; MHC_I_C.
DR Pfam; PF07654; CI-set; 1.
DR Pfam; PF00129; MHC_I; 1.
DR Pfam; PF06623; MHC_I_C; 1.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Transmembrane.
SQ SEQUENCE 362 AA; 40625 MW; BA5699D08181A1FF CRC64;

Query Match 31.2%; Score 113; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 3.4e-100;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 84 TTGYAKANAQTDRLVALNRLNRRYNSAGSHTLQGNQCDMGPDGRLRLRGYHQHAYDGD 143
Db 84 TTGYAKANAQTDRLVALNRLNRRYNSAGSHTLQGNQCDMGPDGRLRLRGYHQHAYDGD 143

QY 144 YISLNEEDLSWTAADTVAQITQRFYEAEYAEFRTYLEGECELELLRRYLENG 196
Db 144 YISLNEEDLSWTAADTVAQITQRFYEAEYAEFRTYLEGECELELLRRYLENG 196

RESULT 14
Q9TPX7
ID Q9TPX7 PRELIMINARY; PRT; 91 AA.
AC Q9TPX7;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE MHC class I antigen (Fragment).
GN Name=Gogo-F;
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]_TaxID=9593;
RP SEQUENCE FROM N.A.
RX Grimsley C.;

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RL Submitted (JUN-1999) to the EMBL/GenBank/DBDJ databases.
DR EMBL; AF159566; AADS1614.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 10354 MW; 2F485A6B6532A61 CRC64;

Query Match 24.0%; Score 87; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.3e-75;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 PPKAHVAHPISDHEATLRCWALGYPAEITLTWQDGEQTDTELVETRPAGDGTPOK 264
Db 1 PPKAHVAHPISDHEATLRCWALGYPAEITLTWQDGEQTDTELVETRPAGDGTPOK 60

QY 265 WAAVVPSEGEQRYTCHVQHEGLPOPL 291
Db 61 WAAVVPSEGEQRYTCHVQHEGLPOPL 87

RESULT 15
Q29958
ID Q29958 PRELIMINARY; PRT; 316 AA.
AC Q29958;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE HLA-C protein (Fragment).
GN Name=HLA-C;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=89122144; PubMed=2314713;
RA Cianetti L., Testa U., Scotto L., La Valle R., Simone A., Bocoli G.,
RA Giannella G., Peschie C., Boncinelli E.;
RT "Three new class I HLA alleles: structure of mRNAs and alternative
RT mechanisms of processing.";
RL Immunogenetics 29:80-91 (1989).
DR EMBL; M24096; AAAS9654.1; -.
DR PIR; C37028; C37028.
DR HSP; Q9MY78; 1M05.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR010339; MHC_I.
DR InterPro; IPR010579; MHC_I_C.
DR Pfam; PF07654; CI-set; 1.
DR Pfam; PF00129; MHC_I; 1.
DR Pfam; PF06623; MHC_I_C; 1.
DR PRINTS; PR01638; MHCCLASSI.
DR ProDom; PD000050; MHC_I; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON_TER 1
FT CHAIN <1 316 Potential.
SQ SEQUENCE 316 AA; 35380 MW; C03B1EC87F75C9BA CRC64;

Query Match 20.2%; Score 73; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.3e-61;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	216	SDHEATLRCWALGFYPAEITLTWQDGEEOQDTELVTETPAGDGTQKWAANVVPSE	275
Db	169	SDHEATLRCWALGFYPAEITLTWQDGEEOQDTELVTETPAGDGTQKWAANVVPSE	228
Qy	276	QRYTCHVQHEGLP	288
Db	229	QRYTCHVQHEGLP	241

Search completed: July 13, 2005, 09:11:49  
Job time : 171 secs

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RESULT 2
US-09-513-999C-4290
; Sequence 4290, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4290
; LENGTH: 120
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -17...-1
; OTHER INFORMATION: score 9.3
; OTHER INFORMATION: seq SLLLLSGALALT/DT
US-09-513-999C-4290

Query Match          36.1%; Score 99; DB 4; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.1e-90; Mismatches 0; Indels 0; Gaps 0;
Matches 99; Conservative 0;

QY 1 GSHSLRYSTAVSRGGRGPRVIAVYVDDTQFLRFDSDAAIPRMEPREPWVQEGPQYW 60
Db 22 GSHSLRYSTAVSRGGRGPRVIAVYVDDTQFLRFDSDAAIPRMEPREPWVQEGPQYW 81

QY 61 EWTGYAKANAQTRVALNRLRRYNQSEAGSHTLQGMN 99
Db 82 EWTGYAKANAQTRVALNRLRRYNQSEAGSHTLQGMN 120

RESULT 3
US-08-222-851-1
; Sequence 1, Application US/08222851
; Patent No. 5723128
; GENERAL INFORMATION:
; APPLICANT: CLAYBERGER, CAROL A.
; APPLICANT: KRENSKI, ALAN M.
; APPLICANT: PARHAM, PETER
; TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,851
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLMAN, ROBERT A.
; REGISTRATION NUMBER: 36,217
; REFERENCE/DOCKET NUMBER: 28500-20200.22
; TELECOMMUNICATION INFORMATION:

US-09-819-371-5.ra1
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 494-0792
; TELEX: 90-4030 MRSNFOERSWHS
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-222-851-1

Query Match          16.1%; Score 44; DB 1; Length 274;
Best Local Similarity 100.0%; Pred. No. 1.6e-35; Mismatches 0; Indels 0; Gaps 0;
Matches 44; Conservative 0;

QY 224 QTQDTVELVETRPAGDGTFOKWAADVVPVSGEQRVYTCVHQHEGLP 267
Db 224 QTQDTVELVETRPAGDGTFOKWAADVVPVSGEQRVYTCVHQHEGLP 267

RESULT 4
US-09-949-016-6620
; Sequence 6620, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6620
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6620

Query Match          15.7%; Score 43; DB 4; Length 358;
Best Local Similarity 100.0%; Pred. No. 2e-34; Mismatches 0; Indels 0; Gaps 0;
Matches 43; Conservative 0;

QY 225 TQDTVELVETRPAGDGTFOKWAADVVPVSGEQRVYTCVHQHEGLP 267
Db 246 TQDTVELVETRPAGDGTFOKWAADVVPVSGEQRVYTCVHQHEGLP 288

RESULT 5
US-09-949-016-8370
; Sequence 8370, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 8370  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-8370

Query Match 15.7%; Score 43; DB 4; Length 360;  
Best Local Similarity 100.0%; Pred. No. 2e-34;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 TQTELVEPRAGDGTQKWAADVVPSEGEQRYTCHVQHEGLP 267  
|||||

Db 248 TQTELVEPRAGDGTQKWAADVVPSEGEQRYTCHVQHEGLP 290  
|||||

## RESULT 6

US-08-406-057-9  
; Sequence 9, Application US/08406057  
; Patent No. 5856442

## GENERAL INFORMATION:

APPLICANT: CAROSELLA, EDGARDO D  
APPLICANT: MOREAU, PHILIPPE  
APPLICANT: GLUCKMAN, ELIANE  
APPLICANT: KIRSZENBAUM, MAREK

TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G  
TITLE OF INVENTION: GENE AND THEIR APPLICATIONS

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
CITY: ARLINGTON  
STATE: VIRGINIA

COUNTRY: USA

ZIP: 2202

COMPUTER READABLE FORM:

MEDIUM TYPE: Tape

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/406,057

FILING DATE: 17-MAR-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 94 03179

FILING DATE: 18-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 846-331-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 117 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-406-057-9

Query Match 14.2%; Score 39; DB 2; Length 117;  
Best Local Similarity 100.0%; Pred. No. 6.8e-31;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ELVETPRAGDGTQKWAADVVPSEGEQRYTCHVQHEGLP 267  
|||||

Db 51 ELVETPRAGDGTQKWAADVVPSEGEQRYTCHVQHEGLP 89  
|||||

## RESULT 7

US-08-958-316-9

; Sequence 9, Application US/08958316

; Patent No. 6291659

; GENERAL INFORMATION:

APPLICANT: CAROSELLA, EDGARDO D

APPLICANT: MOREAU, PHILIPPE

APPLICANT: GLUCKMAN, ELIANE

APPLICANT: KIRSZENBAUM, MAREK

TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G

TITLE OF INVENTION: GENE AND THEIR APPLICATIONS

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: USA

ZIP: 2202

COMPUTER READABLE FORM:

MEDIUM TYPE: Tape

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/958,316

FILING DATE: 27-OCT-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 94 03179

FILING DATE: 18-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 0846-0437-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 117 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-958-316-9

Query Match

Best Local Similarity 14.2%; Score 39; DB 3; Length 117;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ELVETPRAGDGTQKWAADVVPSEGEQRYTCHVQHEGLP 267  
|||||

Db 51 ELVETPRAGDGTQKWAADVVPSEGEQRYTCHVQHEGLP 89  
|||||

## RESULT 8

US-08-406-057-8

; Sequence 8, Application US/08406057

; Patent No. 5856442

; GENERAL INFORMATION:

APPLICANT: CAROSELLA, EDGARDO D

APPLICANT: MOREAU, PHILIPPE

APPLICANT: GLUCKMAN, ELIANE

APPLICANT: KIRSZENBAUM, MAREK

TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G

TITLE OF INVENTION: GENE AND THEIR APPLICATIONS

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: USA  
ZIP: 2202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Tape  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/406,057  
FILING DATE: 17-MAR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 94 03179  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 846-331-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 145 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-406-057-8

Query Match 14.2%; Score 39; DB 2; Length 145;  
Best Local Similarity 100.0%; Pred. No. 8.2e-31;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 267  
|||||  
DB 79 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 117  
|||||

RESULT 9  
US-08-316-8  
Sequence 8, Application US/08958316  
Patent No. 6291659  
GENERAL INFORMATION:  
APPLICANT: CAROSELLA, EDGARDO D  
APPLICANT: MOREAU, PHILIPPE  
APPLICANT: GLUCKMAN, ELIANE  
APPLICANT: KIRSZENBAUM, MAKEK  
TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G  
INVENTION: GENE AND THEIR APPLICATIONS  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: USA  
ZIP: 2202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Tape  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/958,316  
FILING DATE: 27-OCT-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 94 03179  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F

REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 0846-0437-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 145 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-958-316-8

Query Match 14.2%; Score 39; DB 3; Length 145;  
Best Local Similarity 100.0%; Pred. No. 8.2e-31;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 267  
|||||  
DB 79 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 117  
|||||

RESULT 10  
US-09-949-016-6176  
Sequence 6176, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6176  
LENGTH: 338  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-6176

Query Match 14.2%; Score 39; DB 4; Length 338;  
Best Local Similarity 100.0%; Pred. No. 1.8e-30;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 267  
|||||  
DB 253 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 291  
|||||

RESULT 11  
US-09-949-016-8636  
Sequence 8636, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03

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: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: fastSEQ for Windows Version
: SEQ ID NO 8636
: LENGTH: 339
: TYPE: PRT
: ORGANISM: Human
US-09-949-016-8636

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Query Match	14.2%;	Score 39;	DB 4;	Length 339;
Best Local Similarity	100.0%;	Pred. No. 1.8e-30;		
Matches 39;	Conservative 0;	Mismatches 0;	Indels	
Qy	229	ELVETRPAGDGTGFKWAAVVPVSGEEORYTCHVQHEGLP	267	
Db	254	ELVETRPAGDGTGFKWAAVVPVSGEEORYTCHVQHEGLP	292	

RESULT 12  
US-08-484-905-79  
; Sequence 79, Application US/08484905  
; Patent No. 5976551  
; GENERAL INFORMATION:  
; APPLICANT: Mottez, Estelle  
; APPLICANT: Abastado, Jean-Pierre  
; APPLICANT: Kourilsky, Philippe  
; TITLE OF INVENTION: An Altered Major Histocompatibility  
; TITLE OF INVENTION: Complex (MHC) Determinant and Met  
; TITLE OF INVENTION: Determinant  
; NUMBER OF SEQUENCES: 127  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESS: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington

STATE: D.C.  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS-/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,905  
FILING DATE: 07-JUNE-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION NUMBER: US 07/801,818  
FILING DATE: 05-DEC-1991  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,473  
FILING DATE: 15-NOV-1991  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Potter, Jane E. R.  
REGISTRATION NUMBER: 33,332  
REFERENCE/DOCKET NUMBER: 03495.0106-03000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 289 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-484-905-79

Query Match 10.9%; Score 30; DB 2; Length 289;  
Best Local Similarity 100.0%; Pred. No. 1.3e-21;  
Matches 30; Conservative 0; Mismatches 0; Indels

Qy 226 QDTELVETRPAGDGTGFKWAAVVVPSGEEQ 255  
Db 226 QDTELVETRPAGDGTGFKWAAVVVPSGEEQ 255

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RESULT 13
US-08-481-985B-79
; Sequence 79, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Parabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315

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COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/481,985B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,818  
FILING DATE: 05-DEC-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,473  
FILING DATE: 15-NOV-1991  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0106-04000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 289 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-481-985B-79

Query Match	10.9%;	Score 30;	DB 3;	Length 289;
Best Local Similarity	100.0%;	Pred. No. 1.3e-21;		
Matches 30;	Conservative	0;	Mismatches 0;	Indels 0;
			0;	Gaps 0;

**Qy**

226 QTELVETRPAGDGT**FQKAAVVVPSEEQ** 255  
| | | | | | | | | | | | |  
**Dβ**

226 QTELVETRPAGDGT**FQKAAVVVPSEEQ** 255  
| | | | | | | | | | | | |

RESULT 14  
US-08-370-476-79  
; Sequence 79, Application US/08370476  
; Patent No. 6153408  
; GENERAL INFORMATION:  
; APPLICANT: Mottez, Estelle  
; APPLICANT: Abastado, Jean-Pierre  
; APPLICANT: Kourilsky, Phillipe

RESULT 15  
US-08-484-905-105  
; Sequence 105, Application US/08484905  
; Patent No. 5976551  
; GENERAL INFORMATION:  
; APPLICANT: Mottez, Etelle  
; APPLICANT: Abastado, Jean-Pierre  
; APPLICANT: Kourilsky, Philippe  
; TITLE OF INVENTION: An Altered Major Histocompatibility  
; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the  
; TITLE OF INVENTION: Determinant  
; NUMBER OF SEQUENCES: 127  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700

```

CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495.0106-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-905-105

Query Match 10.6%; Score 29; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 29; Conservative 0; Mismatches 0; Indels

QY 224 QTQDTVELVETRPAGDGTFKWAAVVPVS 252
DB 224 QTQDTVELVETRPAGDGTFKWAAVVPVS 252

Search completed: July 13, 2005, 09:29:09
Job time : 22.8528 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 13, 2005, 09:02:43 ; Search time 40 Seconds  
(without alignments)  
870.762 Million cell updates/sec

Title: US-09-819-371-4  
Perfect score: 362  
Sequence: 1 MAPRSLLLSGALALTDTW.....QAAVTSAGSGVSLTANKV 362

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	261	72.1	362	2 A60384	MHC class I histoc
2	113	31.2	345	2 S07114	MHC class I histoc
3	73	20.2	316	2 C37028	MHC class I histoc
4	59	16.3	348	2 S29990	histocompatibility
5	44	12.2	275	1 HLHUI0	MHC class I histoc
6	44	12.2	298	2 S44994	class I histocompa
7	44	12.2	313	2 I36958	MHC class I histoc
8	44	12.2	325	2 I54449	MHC class I HLA-Cx
9	44	12.2	332	2 S06424	MHC class I histoc
10	44	12.2	345	2 I68749	MHC class I histoc
11	44	12.2	354	2 I54551	histocompatibility
12	44	12.2	357	2 I36966	MHC class I protei
13	44	12.2	357	2 I36965	MHC class I protei
14	44	12.2	359	1 HLHUI2	MHC class I histoc
15	44	12.2	364	2 S03535	class I histocompa
16	44	12.2	365	2 S01171	class I histocompa
17	44	12.2	365	2 I36961	MHC class I protei
18	44	12.2	365	2 I37476	MHC class I histoc
19	44	12.2	365	2 A47636	MHC class I histoc
20	44	12.2	365	2 I83063	All-2 - human
21	44	12.2	365	2 I56039	HLA-A30.3 precurs
22	44	12.2	365	2 I61856	MHC class I histoc
23	44	12.2	365	2 I37478	MHC class I histoc
24	44	12.2	365	2 I54493	MHC class I histoc
25	44	12.2	365	2 S77963	MHC class I histoc
26	44	12.2	365	2 I38519	MHC class I histoc
27	44	12.2	365	2 I54416	HLA-Aw24 protein -
28	44	12.2	365	2 I38518	HLA-A-0102 allele
29	44	12.2	366	1 HLHUI3	MHC class I histoc

#### ALIGNMENTS

##### RESULT 1

A60384

MHC class I histocompatibility antigen HLA-F alpha chain Dew3 precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 09-Jul-2004  
C;Accession: A60384; JLO147  
R;Lury, D.; Epstein, H.; Holmes, N.  
Int. Immunol. 2, 531-537, 1990

A;Title: The human class I MHC gene HLA-F is expressed in lymphocytes.

A;Reference number: A60384; MUID:91197889; PMID:1707659

A;Accession: A60384

A;Molecule type: DNA

A;Residues: 1-362 <LUR>

A;Cross-references: UNIPROT:P30511

R;Geraghty, D.E.; Wei, X.; Orr, H.T.; Koller, B.H.

J. Exp. Med. 171, 1-18, 1990

A;Title: Human leukocyte antigen F (HLA-F): an expressed HLA gene composed of a class I

A;Reference number: JLO147; MUID:90111605; PMID:1688605

A;Accession: JLO147

A;Molecule type: DNA

A;Residues: 1-362 <GER>

A;Cross-references: GB:X17093; NID:g32223; PIDN:CAA34947.1; PID:g312407

A;Experimental source: lymphoblastoid cell line

C;Genetics:

A;Gene: GDB:HLA-F

A;Cross-references: GDB:125714

A;Map position: 6p21.3-6p21.3

A;Introns: 22/1; 112/1; 204/1; 296/1; 335/1; 346/1; 362/1

C;Superfamily: class I histocompatibility antigen; immunoglobulin homology

C;Keywords: glycoprotein; heterodimer; transmembrane protein

F;1-21/Domain: signal sequence #status predicted <SIG>

F;22-111/Domain: alpha-1<All>

F;78-104/Region: hypervariable

F;112-203/Domain: alpha-2 <AL2>

F;164-192/Region: hypervariable

F;204-295/Domain: alpha-3 <AL3>

F;217-282/Domain: immunoglobulin homology <IMM>

F;107/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 72.1%; Score 261; DB 2; Length 362;

Best Local Similarity 99.7%; Pred. No. 8.1e-249;

Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPRSLLLSGALALTDTWAGSHSLRYSTAVSRRCGRCPRYIAVEYDDTQFLRPDSD 60

DB 1 MAPRSLLLSGALALTDTWAGSHSLRYSTAVSRRCGRCPRYIAVEYDDTQFLRPDSD 60

QY 61 AAIPTREPPWVEQPGQYWTTCGYAKANAQTDVALNLLRRYNQSEAGSHTLQGMN 120

DB 61 AAIPTREPPWVEQPGQYWTTCGYAKANAQTDVALNLLRRYNQSEAGSHTLQGMN 120

QY 121 GCDMPDGRLLRGYHQHAYDGDGYISLNEDLSRWSAATVAQITQRFYEAEBEFTY 180

DB 121 GCDMPDGRLLRGYHQHAYDGDGYISLNEDLSRWSAATVAQITQRFYEAEBEFTY 180

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Db      121 GCDMGPDGRLRGYHQHAYDGRDYISLNEDLSWTAADTVAQITQRFYEAEFYAEFFRTY 180
      |||
QY      181 LEQCELELLRRYLENGLETQRADPPKAVAHHPISDHEATLRCWALGFYPAEITLTWQR 240
      |||
Db      181 LEQCELELLRRYLENGKETLQRADPPKAVAHHPISDHEATLRCWALGFYPAEITLTWQR 240
      |||
QY      241 DGEQOTQDTLQVETRPAGDGTTFQKAAVVVPSGEEQRYTCHVOHEGLPQPLILRWEQSPQ 300
      |||
Db      241 DGEQOTQDTLQVETRPAGDGTTFQKAAVVVPSGEEQRYTCHVOHEGLPQPLILRWEQSPQ 300
      |||
QY      301 PTPPIVIGIVAGLVVLGAVVTGAVAAVMWRKSSDRNRGYSQAAVTDSAQSGVSLTAN 360
      |||
Db      301 PTPPIVIGIVAGLVVLGAVVTGAVAAVMWRKSSDRNRGYSQAAVTDSAQSGVSLTAN 360
      |||
QY      361 KV 362
      ||
Db      361 KV 362
      ||

RESULT 2
S07114
MHC class I histocompatibility antigen Ch28 alpha chain precursor - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C:Accession: S07114
R:Lawlor, D.A.; Ward, F.E.; Ennis, P.D.; Jackson, A.P.; Parham, P.
Nature 335, 268-271, 1988
A:Title: HLA-A and B polymorphisms predate the divergence of humans and chimpanzees.
A:Reference number: S06424; MUID:88319000; PMID:3412487
A:Accession: S07114
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-345 <LAW>
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein; membrane protein
F:217-282/Domain: immunoglobulin homology <IMM>

Query Match      31.2%; Score 113; DB 2; Length 345;
Best Local Similarity 100.0%; Pred. No. 4.7e-103;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      84 TTGYAKANAQTRVALNRLRRYNOSEAGSHYTLQMGNGCDMGPDGRLRGYHQHAYDGRD 143
      |||
Db      84 TTGYAKANAQTRVALNRLRRYNOSEAGSHYTLQMGNGCDMGPDGRLRGYHQHAYDGRD 143
      |||
QY      144 YISLNEDLSWTAADTVAQITQRFYEAEFYAEFFRTYLRGECELLRLRYLENG 196
      |||
Db      144 YISLNEDLSWTAADTVAQITQRFYEAEFYAEFFRTYLRGECELLRLRYLENG 196
      |||

RESULT 3
C37028
MHC class I histocompatibility antigen HLA-C (clone 9) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 14-Feb-1992 #sequence_revision 30-Jan-1993 #text_change 09-Jul-2004
C:Accession: C37028
R:Cianetti, L.; Testa, U.; Scott, L.; La Valle, R.; Simeone, A.; Boccoli, G.; Giannella
Immunogenetics 29, 80-91, 1989
A:Title: Three new class I HLA alleles: structure of mRNAs and alternative mechanisms of
A:Reference number: A37028; MUID:89122144; PMID:2914713
A:Accession: C37028
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-316 <CIA>
A:Cross-references: UNIPROT:Q96F05; UNIPROT:Q29987; UNIPROT:Q9MW34; UNIPROT:O19677; UNIP
C:Genetics:
A:Gene: GDB:HLA-C
A:Cross-references: GDB:119311; OMIM:142840
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
F:170-235/Domain: immunoglobulin homology <IMM>

```

```

Query Match      20.2%; Score 73; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.1e-63;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      216 SDHEATLRCWALGFYPAEITLTWQRDGEQOTQDTLQVETRPAGDGTTFQKAAVVVPSGEE 275
      |||
Db      169 SDHEATLRCWALGFYPAEITLTWQRDGEQOTQDTLQVETRPAGDGTTFQKAAVVVPSGEE 228
      |||
QY      276 QRYTCHVQHEGLP 288
      |||
Db      229 QRYTCHVQHEGLP 241
      |||

RESULT 4
S29990
histocompatibility antigen, HLA-F-like - rhesus macaque
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S29990
R:Bontrop, R.R.
submitted to the EMBL Data Library, February 1993
A:Reference number: S29990
A:Accession: S29990
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-348 <BON>
A:Cross-references: UNIPROT:P33617; EMBL:221819; NID:G98568; PIDN:CAA79885.1; PID:G38565
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
F:219-284/Domain: immunoglobulin homology <IMM>

Query Match      16.3%; Score 59; DB 2; Length 348;
Best Local Similarity 100.0%; Pred. No. 7.3e-50;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      233 EITLTWQRDGEQOTQDTLQVETRPAGDGTTFQKAAVVVPSGEEQRYTCHVQHEGLPQPL 291
      |||
Db      235 EITLTWQRDGEQOTQDTLQVETRPAGDGTTFQKAAVVVPSGEEQRYTCHVQHEGLPQPL 293
      |||

RESULT 5
HLHUI0
MHC class I histocompatibility antigen HLA-A10 alpha chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: B24512
R:Davidson, W.F.; Kress, M.; Khoury, G.; Jay, G.
J. Biol. Chem. 260, 13414-13423, 1985
A:Title: Comparison of HLA class I gene sequences. Derivation of locus-specific oligonuc
A:Reference number: A92500; MUID:86033791; PMID:3863816
A:Accession: B24512
A:Molecule type: DNA
A:Residues: 1-275 <DAV>
A:Cross-references: UNIPROT:P01892; GB:M11887; NID:G184157; PIDN:AA52656.1; PID:G184158
C:Genetics:
A:Gene: GDB:HLA-A
A:Cross-references: GDB:119310; OMIM:142800
A:Map position: 6p21.3-6p21.3
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen
F:130-195/Domain: immunoglobulin homology <IMM>
F:20/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      12.2%; Score 44; DB 1; Length 275;
Best Local Similarity 100.0%; Pred. No. 3.5e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      245 QTQDTLQVETRPAGDGTTFQKAAVVVPSGEEQRYTCHVQHEGLP 288
      |||
Db      158 QTQDTLQVETRPAGDGTTFQKAAVVVPSGEEQRYTCHVQHEGLP 201
      |||

RESULT 6

```

S44994

Class I histocompatibility antigen HLA-Cw6 precursor - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004  
C:Accession: S44994  
R:Margot, M.; Brockstedt, D.; Jenisch, S.  
submitted to the EMBL Data Library, May 1994  
A:Description: New HLA-Cw6 sequence.  
A:Reference number: S44994  
A:Accession: S44994  
A:Molecule type: mRNA  
A:Residues: 1-298 <MAR>  
A:Cross-references: UNIPROT:Q29866; EMBL:Z33459; NID:g488361; PIDN:CAA83881.1; PID:g488361  
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F:1-72/Domain: signal sequence #status predicted <SIG>  
F:73-298/Product: class I histocompatibility antigen HLA-Cw6 (fragment) #status predicted  
F:220-285/Domain: immunoglobulin homology <IMM>

Query Match 12.2%; Score 44; DB 2; Length 298;  
Best Local Similarity 100.0%; Pred. No. 3.8e-35;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLTVETRPAGDGTGFKWAAVVVPSGEQRYTCHVQHEGLP 288  
|||||  
DB 248 QTQDTLTVETRPAGDGTGFKWAAVVVPSGEQRYTCHVQHEGLP 291  
|||||

RESULT 7

I36958  
MHC class I - chimpanzee (fragment)  
C:Species: Pan troglodytes (chimpanzee)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I36958  
R:Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.  
J. Immunol. 142, 3937-3950, 1989  
A:Title: Diversity and diversification of HLA-A,B,C alleles.  
A:Reference number: I36958  
A:Accession: I36958  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-313 <RES>  
A:Cross-references: UNIPROT:Q30989; GB:M24046; NID:g176816; PIDN:AAA3425.1; PID:g176817  
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F:167-232/Domain: immunoglobulin homology <IMM>

Query Match 12.2%; Score 44; DB 2; Length 313;  
Best Local Similarity 100.0%; Pred. No. 4e-35;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLTVETRPAGDGTGFKWAAVVVPSGEQRYTCHVQHEGLP 288  
|||||  
DB 195 QTQDTLTVETRPAGDGTGFKWAAVVVPSGEQRYTCHVQHEGLP 238  
|||||

RESULT 8

I54449  
MHC class I HLA-Cx52 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 21-Jan-2000  
C:Accession: I54449  
R:Takata, H.; Inoko, H.; Ando, A.; Haranaka, M.; Watanabe, B.; Tsuji, K.; Iri, H.  
Immunogenetics 28, 265-270, 1988  
A:Title: Cloning and analysis of HLA class I cDNA encoding a new HLA-C specificity Cx52.  
A:Reference number: I54449; MUID:88330144; PMID:2843461  
A:Accession: I54449  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-325 <RES>  
A:Cross-references: GB:M21963; NID:g188540; PIDN:AAA59847.1; PID:g188541  
C:Genetics:  
A:Gene: GDB:HLA-C  
A:Cross-references: GDB:I19311; OMIM:142840  
A:Map position: 6p21.3-6p21.3

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F:179-244/Domain: immunoglobulin homology <IMM>

Query Match 12.2%; Score 44; DB 2; Length 325;  
Best Local Similarity 100.0%; Pred. No. 4.1e-35;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLTVETRPAGDGTGFKWAAVVVPSGEQRYTCHVQHEGLP 288  
|||||  
DB 207 QTQDTLTVETRPAGDGTGFKWAAVVVPSGEQRYTCHVQHEGLP 250  
|||||

RESULT 9

S06424  
MHC class I histocompatibility antigen Ch25 alpha chain precursor - chimpanzee  
N:Alternate names: MHC Ch1a chain  
C:Species: Pan troglodytes (chimpanzee)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S06424; I36959  
R:Lawlor, D.A.; Ward, F.E.; Ennis, P.D.; Jackson, A.P.; Parham, P.  
Nature 335, 268-271, 1988  
A:Title: HLA-A and B polymorphisms predate the divergence of humans and chimpanzees.  
A:Reference number: S06424; MUID:88319000; PMID:3412487  
A:Accession: S06424  
A:Molecule type: mRNA  
A:Residues: 1-332 <LAW>  
A:Cross-references: UNIPROT:Q30990  
R:Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.  
J. Immunol. 142, 3937-3950, 1989  
A:Title: Diversity and diversification of HLA-A,B,C alleles.  
A:Reference number: I36959; MUID:89235215; PMID:2715840  
A:Accession: I36959  
A:Molecule type: mRNA  
A:Residues: 1-332 <RES>  
A:Cross-references: GB:M24047; NID:g176818; PIDN:AAA35426.1; PID:g553155  
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F:1-24/Domain: signal sequence #status predicted <SIG>  
F:25-114/Domain: alpha-1 #status predicted <EX1>  
F:115-206/Domain: alpha-2 #status predicted <EX2>  
F:220-285/Domain: immunoglobulin homology <IMM>  
F:307-331/Domain: transmembrane #status predicted <TM>  
F:110/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:125-188,227-283/Disulfide bonds: #status predicted

Query Match 12.2%; Score 44; DB 2; Length 332;  
Best Local Similarity 100.0%; Pred. No. 4.2e-35;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLTVETRPAGDGTGFKWAAVVVPSGEQRYTCHVQHEGLP 288  
|||||  
DB 248 QTQDTLTVETRPAGDGTGFKWAAVVVPSGEQRYTCHVQHEGLP 291  
|||||

RESULT 10

I68749  
MHC class I lymphocyte antigen - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 09-Jul-2004  
C:Accession: I68749  
R:Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.  
Immunogenetics 29, 297-307, 1989  
A:Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-B  
A:Reference number: I54457; MUID:89233295; PMID:2714852  
A:Accession: I68749  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-345 <RES>  
A:Cross-references: UNIPROT:Q29963; GB:M28206; NID:g576476; PIDN:AAA57258.1; PID:g57647  
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F:199-264/Domain: immunoglobulin homology <IMM>

Query Match 12.2%; Score 44; DB 2; Length 345;

Best Local Similarity 100.0%; Pred. No. 4.3e-35;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLVELTRPAGDGTGTFQKAAAVVPSGEEQRYTCHVQHEGLP 288  
|||||  
DB 227 QTQDTLVELTRPAGDGTGTFQKAAAVVPSGEEQRYTCHVQHEGLP 270  
|||||

RESULT 11

I54551  
histocompatibility antigen - crab-eating macaque (fragment)  
C/Species: Macaca fascicularis (crab-eating macaque)  
C/Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 09-Jul-2004  
C/Accession: I54551  
R;Boysen, J.E.; McCadam, S.N.; Gallimore, A.; Golos, T.G.; Liu, X.; Gotch, F.M.; Hughes, Immunogenetics 41, 59-68, 1995  
A/Title: The MHC B locus in macaques is polymorphic and is conserved between macaques and  
A/Reference number: I54551; MUID:95104933; PMID:7806297  
A/Accession: I54551  
A/Status: preliminary;  
A/Molecule type: mRNA  
A/Residues: 1-354 <RES>  
A/Cross-references: UNIPROT:Q95513; EMBL:U02976; NID:g413827; PIDN:AAA70050.1; PID:g413828  
C/Superfamily: class I histocompatibility antigen; immunoglobulin homology  
F/209-274/Domain: immunoglobulin homology <IMM>

Query Match 12.2%; Score 44; DB 2; Length 354;  
Best Local Similarity 100.0%; Pred. No. 4.4e-35;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLVELTRPAGDGTGTFQKAAAVVPSGEEQRYTCHVQHEGLP 288  
|||||  
DB 237 QTQDTLVELTRPAGDGTGTFQKAAAVVPSGEEQRYTCHVQHEGLP 280  
|||||

RESULT 12

I36966  
MHC class I protein - chimpanzee (fragment)  
C/Species: Pan troglodytes (chimpanzee)  
C/Date: 04-Oct-1996 #sequence\_revision 04-Oct-1996 #text\_change 09-Jul-2004  
C/Accession: I36966  
R;Chen, Z.W.; Hughes, A.L.; Ghim, S.H.; Letvin, N.L.; Watkins, D.I. Immunogenetics 38, 238-240, 1993  
A/Title: Two more chimpanzee Patr-A locus alleles related to the HLA-A1/A3/A11 family.  
A/Reference number: I36965; MUID:93279743; PMID:8505066  
A/Accession: I36966  
A/Status: preliminary; translated from GB/EMBL/DBDB  
A/Molecule type: mRNA  
A/Residues: 1-357 <RES>  
A/Cross-references: UNIPROT:Q9MKL2; UNIPROT:Q30993; GB:M55245; NID:g176836; PIDN:AAA0368  
C/Genetics:

Query Match 12.2%; Score 44; DB 2; Length 357;  
Best Local Similarity 100.0%; Pred. No. 4.5e-35;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLVELTRPAGDGTGTFQKAAAVVPSGEEQRYTCHVQHEGLP 288  
|||||  
DB 240 QTQDTLVELTRPAGDGTGTFQKAAAVVPSGEEQRYTCHVQHEGLP 283  
|||||

RESULT 13

I36965  
MHC class I protein (A5) - chimpanzee (fragment)  
C/Species: Pan troglodytes (chimpanzee)  
C/Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004  
C/Accession: I36965  
R;Chen, Z.W.; Hughes, A.L.; Ghim, S.H.; Letvin, N.L.; Watkins, D.I. Immunogenetics 38, 238-240, 1993  
A/Title: Two more chimpanzee Patr-A locus alleles related to the HLA-A1/A3/A11 family.



Query Match 12.2%; Score 44; DB 2; Length 364;

Best Local Similarity 100.0%; Pred. No. 4.6e-35;

Matches	44;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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Qy 245 QTQDTLVELTRPAGDTFQKWAAVVVPSSGEEQRYTCHVQHEGLP 288

Db 247 QTQDTLVELTRPAGDGTFFQKWAAVVPSGEEQRYTCHVQHEGLP 290

Search completed: July 13, 2005, 09:15:25

Job time : 41 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model.

Run on: July 13, 2005, 09:25:40 ; Search time 120.47 Seconds  
(without alignments)  
878.681 Million cell updates/sec

Title: US-09-819-371-5  
Perfect score: 274  
Sequence: 1 GSHSLRYFTAVSRPGRGP.....QRYTCHVQHGLPQPLILRW 274

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1726220 seqs, 386332138 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 1726220

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:  
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3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
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6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
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11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
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16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*  
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19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	274	100.0	274	11 US-09-819-371-5	Sequence 5, Appl1
2	274	100.0	362	15 US-10-257-021-82	Sequence 82, Appl
3	274	100.0	422	16 US-10-408-765A-1887	Sequence 1887, Ap
4	241	88.0	271	9 US-09-925-301-1431	Sequence 1431, Ap
5	175	63.9	362	11 US-09-819-371-4	Sequence 4, Appl1
6	119	43.4	215	11 US-09-819-371-6	Sequence 6, Appl1
7	70	25.5	186	15 US-10-264-049-4063	Sequence 4063, Ap
8	68	24.8	96	14 US-10-029-386-30718	Sequence 30718, A
9	44	16.1	77	14 US-10-029-386-34273	Sequence 34273, A
10	44	16.1	91	14 US-10-029-386-31089	Sequence 31089, A
11	44	16.1	104	9 US-09-925-302-835	Sequence 835, App

12	16.1	104	10	US-09-925-302-835	Sequence 835, App
13	16.1	365	17	US-10-741-600-941	Sequence 941, App
14	16.1	476	16	US-10-430-984-16	Sequence 16, Appl
15	15.7	500	16	US-10-430-984-15	Sequence 15, Appl
16	14.6	78	14	US-10-029-386-30752	Sequence 30752, A
17	14.6	371	15	US-10-085-198-72	Sequence 72, Appl
18	14.6	371	15	US-10-210-172-156	Sequence 156, App
19	14.2	91	9	US-09-864-761-38005	Sequence 38005, A
20	14.2	92	15	US-10-380-880-5	Sequence 5, Appl1
21	14.2	169	16	US-10-741-601-383	Sequence 383, App
22	14.2	169	17	US-10-741-601-1135	Sequence 1135, Ap
23	14.2	198	16	US-10-741-601-387	Sequence 387, App
24	14.2	198	17	US-10-741-600-1143	Sequence 1143, Ap
25	14.2	234	15	US-10-380-880-8	Sequence 8, Appl1
26	14.2	251	16	US-10-741-601-384	Sequence 384, App
27	14.2	251	17	US-10-741-600-1142	Sequence 1142, Ap
28	14.2	284	15	US-10-104-047-3648	Sequence 3648, Ap
29	14.2	326	15	US-10-380-880-7	Sequence 7, Appl1
30	14.2	338	16	US-10-741-601-380	Sequence 380, App
31	14.2	338	16	US-10-741-601-388	Sequence 388, App
32	14.2	338	17	US-10-741-600-1134	Sequence 1134, Ap
33	14.2	338	17	US-10-741-600-1138	Sequence 1138, Ap
34	14.2	338	17	US-10-482-029-1110	Sequence 110, App
35	14.2	343	16	US-10-741-601-379	Sequence 379, App
36	14.2	343	17	US-10-741-600-1139	Sequence 1139, Ap
37	14.2	379	15	US-10-093-463-78	Sequence 78, Appl
38	14.2	379	15	US-10-210-172-160	Sequence 160, App
39	13.9	145	9	US-09-810-560-8	Sequence 8, Appl1
40	13.1	45	14	US-10-029-386-28883	Sequence 28883, A
41	11.7	91	9	US-09-864-761-35461	Sequence 35461, A
42	11.7	110	9	US-09-796-692-799	Sequence 799, App
43	11.7	110	9	US-09-796-692-2139	Sequence 2139, App
44	11.7	110	14	US-10-040-862-799	Sequence 799, App
45	11.7	110	14	US-10-040-862-2139	Sequence 2139, App

ALIGNMENTS

RESULT 1  
US-09-819-371-5  
; Sequence 5, Application US/09819371  
; Publication No. US20040053344A1  
; GENERAL INFORMATION:  
; APPLICANT: Egawa, Kohji  
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Ca  
; FILE OF INVENTION: Using Thereof  
; FILE REFERENCE: 30815  
; CURRENT APPLICATION NUMBER: US/09/819,371  
; CURRENT FILING DATE: 2002-03-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 274  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-819-371-5

Query Match	100.0%	Score	274	DB	11	Length	274
Best Local Similarity	100.0%	Pred. No.	2.4e-260				
Matches	274	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
QY	1	GSHSLRYFTAVSRPGRGP	RYIAVEYVD	TQFLRFDSDAAI	PRMPEP	FWVEQEGPQYW	60
Db	1	GSHSLRYFTAVSRPGRGP	RYIAVEYVD	TQFLRFDSDAAI	PRMPEP	FWVEQEGPQYW	60
QY	61	EWTTGYAKANAQDTRVALNLLRRY	NQNSAGSH	TLCGMGNC	MDPGDRL	LRGHYHAYDG	120
Db	61	EWTTGYAKANAQDTRVALNLLRRY	NQNSAGSH	TLCGMGNC	MDPGDRL	LRGHYHAYDG	120
QY	121	KDYISLNEDLRSWTAADTVAQITQ	RYEABEYAE	EEFTYLEG	ECLELLR	RYLNGKETLQ	180
Db	121	KDYISLNEDLRSWTAADTVAQITQ	RYEABEYAE	EEFTYLEG	ECLELLR	RYLNGKETLQ	180



Db 148 KQVSLNEDLRSWTAADTVAAITQRFYAEYAEFFTYLGECELELLRRYLENGKETLQ 207  
QY 181 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQRDGESEQTQDTLTVETRPAGDGT 240  
Db 208 RADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQRDGESEQTQDTLTVETRPAGDGT 267  
QY 241 F 241  
Db 268 F 268

## RESULT 5

US-09-819-371-4  
; Sequence 4, Application US/09819371  
; Publication No. US20040053344A1  
; GENERAL INFORMATION:  
; APPLICANT: Egawa, Kohji  
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can  
; TITLE OF INVENTION: Using Thereof  
; FILE REFERENCE: 30815  
; CURRENT APPLICATION NUMBER: US/09/819,371  
; CURRENT FILING DATE: 2002-03-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 4  
; LENGTH: 362  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-819-371-4

Query Match 63.9%; Score 175; DB 11; Length 362;  
Best Local Similarity 100.0%; Pred. No. 5e-163;  
Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSHSLRYFSAVSRPGRGEPRIYAVEYDDTQFLRFDSDAAIPRMEPREPWVQSGPQYW 60  
Db 22 GSHSLRYFSAVSRPGRGEPRIYAVEYDDTQFLRFDSDAAIPRMEPREPWVQSGPQYW 81  
QY 61 EWTGKAKANAQTRDVALRNLRRYNSQSEAGSHTLQMGNCMDGPDGRLRLRGYHQHAYDG 120  
Db 82 EWTGKAKANAQTRDVALRNLRRYNSQSEAGSHTLQMGNCMDGPDGRLRLRGYHQHAYDG 141  
QY 121 KQVSLNEDLRSWTAADTVAAITQRFYAEYAEFFTYLGECELELLRRYLENG 175  
Db 142 KQVSLNEDLRSWTAADTVAAITQRFYAEYAEFFTYLGECELELLRRYLENG 196

## RESULT 6

US-09-819-371-6  
; Sequence 6, Application US/09819371  
; Publication No. US20040053344A1  
; GENERAL INFORMATION:  
; APPLICANT: Egawa, Kohji  
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can  
; TITLE OF INVENTION: Using Thereof  
; FILE REFERENCE: 30815  
; CURRENT APPLICATION NUMBER: US/09/819,371  
; CURRENT FILING DATE: 2002-03-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 6  
; LENGTH: 215  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-819-371-6

Query Match 43.4%; Score 119; DB 11; Length 215;  
Best Local Similarity 100.0%; Pred. No. 3.1e-108;  
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 119 DGKDYISLNEDLRSWTAADTVAAITQRFYAEYAEFFTYLGECELELLRRYLENGKET 178  
Db 97 DGKDYISLNEDLRSWTAADTVAAITQRFYAEYAEFFTYLGECELELLRRYLENGKET 156

QY 179 LQADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQRDGESEQTQDTLTVETRPAG 237  
Db 157 LQADPPKARVAHPISDHEATLRCWALGFYPAEITLTWQRDGESEQTQDTLTVETRPAG 215

## RESULT 7

US-10-264-049-4063  
; Sequence 4063, Application US/10264049  
; Publication No. US20040005579A1  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PA133PI  
; CURRENT APPLICATION NUMBER: US/10/264,049  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/18569  
; PRIOR FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: US 60/209,467  
; PRIOR FILING DATE: 2000-06-07  
; NUMBER OF SEQ ID NOS: 4360  
; SOFTWARE: Patent in Ver. 3.1  
; SEQ ID NO 4063  
; LENGTH: 186  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: MISC FEATURE  
; LOCATION: (76)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (77)  
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; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (86)  
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; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (107)  
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; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (123)  
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; NAME/KEY: MISC FEATURE  
; LOCATION: (124)  
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; LOCATION: (136)  
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; NAME/KEY: MISC FEATURE  
; LOCATION: (148)  
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; NAME/KEY: MISC FEATURE  
; LOCATION: (174)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
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; NAME/KEY: MISC FEATURE  
; LOCATION: (175)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
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; NAME/KEY: MISC FEATURE  
; LOCATION: (176)

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; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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; NAME/KEY: MISC FEATURE
; LOCATION: (180)
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US-10-264-049-4063

Query Match      25.5%; Score 70; DB 15; Length 186;
Best Local Similarity 100.0%; Pred. No. 3.5e-60;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 66 YAKANAQTRVALNLLRRYNQSEAGSHTLQGNQCDMGDPGRLRGVHQAHDGKDYIS 125
Db 1 YAKANAQTRVALNLLRRYNQSEAGSHTLQGNQCDMGDPGRLRGVHQAHDGKDYIS 60
QY 126 LNEDLRSWTA 135
Db 61 LNEDLRSWTA 70

RESULT 8
US-10-029-386-30718
; Sequence 30718, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 30718
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR6.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12
; OTHER INFORMATION: SWISSPROT HIT: P30511, EVALUE 2.00e-52
US-10-029-386-30718

Query Match      24.8%; Score 68; DB 14; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.8e-58;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 DPPKAHVHHPISDHEATLRCWALGFYPAEITLTWQRDGEETQDTLVELTRPAGDGTGQ 242
Db 2 DPPKAHVHHPISDHEATLRCWALGFYPAEITLTWQRDGEETQDTLVELTRPAGDGTGQ 61
QY 243 KWAAVVVP 250
Db 62 KWAAVVVP 69

RESULT 9
US-10-029-386-34273
; Sequence 34273, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
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; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34273
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR6.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 53
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.4
; OTHER INFORMATION: SWISSPROT HIT: P30507, EVALUE 6.00e-42
US-10-029-386-34273

Query Match      16.1%; Score 44; DB 14; Length 77;
Best Local Similarity 100.0%; Pred. No. 5.4e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVELTRPAGDGTGFKWAAVVVPSGGEORYTCHVQHEGLP 267
Db 25 QTQDTLVELTRPAGDGTGFKWAAVVVPSGGEORYTCHVQHEGLP 68

RESULT 10
US-10-029-386-31089
; Sequence 31089, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 31089
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004204.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1
; OTHER INFORMATION: SWISSPROT HIT: P30509, EVALUE 1.00e-52
US-10-029-386-31089

Query Match      16.1%; Score 44; DB 14; Length 91;
Best Local Similarity 100.0%; Pred. No. 6.3e-35;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVELTRPAGDGTGFKWAAVVVPSGGEORYTCHVQHEGLP 267
Db 41 QTQDTLVELTRPAGDGTGFKWAAVVVPSGGEORYTCHVQHEGLP 84

RESULT 11
US-09-925-302-835
; Sequence 835, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
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; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 835

; LENGTH: 104

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (95)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-925-302-835

Query Match

16.1%; Score 44; DB 9; Length 104;

Best Local Similarity 100.0%; Pred. No. 7.1e-35;

Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 267

Db 32 QTQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 75

RESULT 12

US-09-925-302-835

; Sequence 835, Application US/09925302

; Publication No. US20030064072A9

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA104

; CURRENT APPLICATION NUMBER: US/09/925,302

; CURRENT FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05918

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 896

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 835

; LENGTH: 104

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (95)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-925-302-835

Query Match

16.1%; Score 44; DB 10; Length 104;

Best Local Similarity 100.0%; Pred. No. 7.1e-35;

Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 267

Db 32 QTQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 75

RESULT 13

US-10-741-600-941

; Sequence 941, Application US/10741600

; Publication No. US20050026169A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001499

; CURRENT APPLICATION NUMBER: US/10/741,600

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 73997

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 941

; LENGTH: 365

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-741-600-941

Query Match 16.1%; Score 44; DB 17; Length 365;  
Best Local Similarity 100.0%; Pred. No. 2.2e-34;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 QTQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 267

Db 248 QTQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 291

RESULT 14

US-10-430-984-16

; Sequence 16, Application US/10430984

; Publication No. US20040225112A1

; GENERAL INFORMATION:

; APPLICANT: The Board of Trustees of the University of Arkansas

; APPLICANT: Crew, Mark D

; TITLE OF INVENTION: Genes Encoding Single Chain Human Leukocyte Antigen E (HLA-E)

; TITLE OF INVENTION: Proteins to Prevent Natural Killer Cell-Mediated Cytotoxicity

; FILE REFERENCE: 8793-53098

; CURRENT APPLICATION NUMBER: US/10/430,984

; CURRENT FILING DATE: 2003-05-09

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 16

; LENGTH: 476

; TYPE: PRT

; ORGANISM: human leukocyte antigen E-Single chain dimer

US-10-430-984-16

Query Match

15.7%; Score 43; DB 16; Length 476;

Best Local Similarity 100.0%; Pred. No. 2.6e-33;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 TQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 267

Db 364 TQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 406

RESULT 15

US-10-430-984-15

; Sequence 15, Application US/10430984

; Publication No. US20040225112A1

; GENERAL INFORMATION:

; APPLICANT: The Board of Trustees of the University of Arkansas

; APPLICANT: Crew, Mark D

; TITLE OF INVENTION: Genes Encoding Single Chain Human Leukocyte Antigen E (HLA-E)

; TITLE OF INVENTION: Proteins to Prevent Natural Killer Cell-Mediated Cytotoxicity

; FILE REFERENCE: 8793-53098

; CURRENT APPLICATION NUMBER: US/10/430,984

; CURRENT FILING DATE: 2003-05-09

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 15

; LENGTH: 500

; TYPE: PRT

; ORGANISM: human leukocyte antigen E-Single chain Trimer

US-10-430-984-15

Query Match

15.7%; Score 43; DB 16; Length 500;

Best Local Similarity 100.0%; Pred. No. 2.7e-33;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 TQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 267

Db 388 TQDTLVETRPAGDGTFOKAAVVVPSGEEQRYTCHVQHEGLP 430

Search completed: July 13, 2005, 09:46:00  
Job time : 121.47 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 09:09:04 ; Search time 43 Seconds  
(without alignments)  
628.441 Million cell updates/sec

Title: US-09-819-371-4  
Perfect score: 362  
Sequence: 1 MAPRSLLLSGALALTDWT.....QAATVDSAGQGVSLTANKV 362

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545.

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	196	54.1	362	4	US-09-949-016-8242
2	120	33.1	120	4	US-09-513-999C-4290
3	44	12.2	274	1	US-08-222-851-1
4	43	11.9	358	4	US-09-949-016-6620
5	43	11.9	360	4	US-09-949-016-8370
6	39	10.8	117	2	US-08-406-057-9
7	39	10.8	117	3	US-08-958-316-9
8	39	10.8	145	2	US-08-406-057-8
9	39	10.8	145	3	US-08-958-316-8
10	39	10.8	338	4	US-09-949-016-6176
11	39	10.8	339	4	US-09-949-016-8636
12	30	8.3	289	2	US-08-484-905-79
13	30	8.3	289	3	US-08-481-985B-79
14	30	8.3	289	3	US-08-370-476-79
15	29	8.0	274	2	US-08-484-905-105
16	29	8.0	274	2	US-08-484-905-107
17	29	8.0	274	2	US-08-484-905-108
18	29	8.0	274	3	US-08-481-985B-105
19	29	8.0	274	3	US-08-481-985B-107
20	29	8.0	274	3	US-08-481-985B-108
21	29	8.0	274	3	US-08-370-476-105
22	29	8.0	274	3	US-08-370-476-107
23	29	8.0	274	3	US-08-370-476-108
24	29	8.0	341	3	US-08-890-719-38
25	29	8.0	365	2	US-08-484-905-97
26	29	8.0	365	2	US-08-484-905-98
27	29	8.0	365	2	US-08-484-905-99

28	29	8.0	365	2	US-08-484-905-100	Sequence 100, App
29	29	8.0	365	2	US-08-484-905-101	Sequence 101, App
30	29	8.0	365	3	US-08-481-985B-97	Sequence 97, Appl
31	29	8.0	365	3	US-08-481-985B-98	Sequence 98, Appl
32	29	8.0	365	3	US-08-481-985B-99	Sequence 99, Appl
33	29	8.0	365	3	US-08-481-985B-100	Sequence 100, App
34	29	8.0	365	3	US-08-481-985B-101	Sequence 101, App
35	29	8.0	365	3	US-08-652-265-23	Sequence 23, Appl
36	29	8.0	365	3	US-08-834-497A-23	Sequence 23, Appl
37	29	8.0	365	3	US-08-370-476-97	Sequence 97, Appl
38	29	8.0	365	3	US-08-370-476-98	Sequence 98, Appl
39	29	8.0	365	3	US-08-370-476-99	Sequence 99, Appl
40	29	8.0	365	3	US-08-370-476-100	Sequence 100, App
41	29	8.0	365	3	US-08-370-476-101	Sequence 101, App
42	29	8.0	365	3	US-09-503-444A-23	Sequence 23, Appl
43	27	7.5	184	2	US-08-484-905-83	Sequence 83, Appl
44	27	7.5	184	3	US-08-481-985B-83	Sequence 83, Appl
45	27	7.5	184	3	US-08-370-476-83	Sequence 83, Appl

ALIGNMENTS

RESULT 1  
US-09-949-016-8242  
; Sequence 8242, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8242  
; LENGTH: 362  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-8242

Query Match	54.1%	Score 196;	DB 4;	Length 362;
Best Local Similarity	100.0%;	Pred. No. 9.5e-178;		
Matches 196;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MAPRSLLLSGALALTDWTAGSHSLRYSTAVSRGCGEPRIAYVEYDDTQFLRFDSD	60	
Db	1	MAPRSLLLSGALALTDWTAGSHSLRYSTAVSRGCGEPRIAYVEYDDTQFLRFDSD	60	
Qy	61	AALPRMEPREPWEOGPGQYWEWTTGYAKANAQTDVRLNLLRRYNSAGSHHTLOGMN	120	
Db	61	AALPRMEPREPWEOGPGQYWEWTTGYAKANAQTDVRLNLLRRYNSAGSHHTLOGMN	120	
Qy	121	GCDMGPDGRLRLRYHQHAYDGDYIISLNEDLRSWTAAATVAQITQRFYAEVEAEPRTY	180	
Db	121	GCDMGPDGRLRLRYHQHAYDGDYIISLNEDLRSWTAAATVAQITQRFYAEVEAEPRTY	180	
Qy	181	LEGECELELRRYLENG	196	
Db	181	LEGECELELRRYLENG	196	

RESULT 2  
US-09-513-999C-4290  
; Sequence 4290, Application US/09513999C  
; Patent No. 6783961

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; SEQUENCE CHARACTERISTICS:  
; LENGTH: 274 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-222-851-1
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Query Match 12.2%; Score 44; DB 1; Length 274;  
Best Local Similarity 100.0%; Pred. No. 1.4e-33;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLVELTRPADGTFQKAAVWVPSSGEQRVTCHVQHEGLP 288  
| | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 224 QTQDTLVELTRPADGTFQKAAVWVPSSGEQRVTCHVQHEGLP 267  
| | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 4  
US-09-949-016-6620  
; Sequence 6620, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6620  
; LENGTH: 358  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6620

Query Match 11.9%; Score 43; DB 4; Length 358;  
Best Local Similarity 100.0%; Pred. No. 1.6e-32;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 TQTDELVELTRPADGTFQKAAVWVPSSGEQRVTCHVQHEGLP 288  
| | | | | | | | | | | | | | | | | | | | | | | | | |  
DB 246 TQTDELVELTRPADGTFQKAAVWVPSSGEQRVTCHVQHEGLP 288  
| | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 5  
US-09-949-016-8370  
; Sequence 8370, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8370  
; LENGTH: 360  
; TYPE: PRT  
; ORGANISM: Human



COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/406,057  
FILING DATE: 17-MAR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 94 03179  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 846-331-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 145 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-406-057-8

Query Match 10.8%; Score 39; DB 2; Length 145;  
Best Local Similarity 100.0%; Pred. No. 4.3e-29;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 288  
|||||  
DB 79 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 117  
|||||

RESULT 9  
US-09-819-371-4  
; Sequence 8, Application US/08958316  
; Patent No. 6291659  
; GENERAL INFORMATION:  
; APPLICANT: CAROSELLA, EDGARDO D  
; APPLICANT: MOREAU, PHILIPPE  
; APPLICANT: GLUCKMAN, ELIANE  
; APPLICANT: KIRSZENBAUM, MAREK  
; TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: USA  
; ZIP: 2202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Tape  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/958,316  
FILING DATE: 27-OCT-1997  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 94 03179  
FILING DATE: 18-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 0846-0437-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 145 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-958-316-8

Query Match 10.8%; Score 39; DB 3; Length 145;  
Best Local Similarity 100.0%; Pred. No. 4.3e-29;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 288  
|||||  
DB 79 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 117  
|||||

RESULT 10  
US-09-949-016-6176  
; Sequence 6176, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6176  
; LENGTH: 338  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6176

Query Match 10.8%; Score 39; DB 4; Length 338;  
Best Local Similarity 100.0%; Pred. No. 9.7e-29;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 288  
|||||  
DB 253 ELVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 291  
|||||

RESULT 11  
US-09-949-016-8636  
; Sequence 8636, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 8636  
LENGTH: 339  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-8636

Query Match 10.8%; Score 39; DB 4; Length 339;  
Best Local Similarity 100.0%; Pred. No. 9.7e-29;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 ELVETRPAGDGTQKWAADVVPGEQRYTCHVQHEGLP 288  
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DB 254 ELVETRPAGDGTQKWAADVVPGEQRYTCHVQHEGLP 292  
|||||

## RESULT 12

US-08-484-905-79  
Sequence 79, Application US/08484905  
Patent No. 5976551

## GENERAL INFORMATION:

APPLICANT: Mottez, Estelle  
APPLICANT: Abastado, Jean-Pierre  
APPLICANT: Kourilsky, Philippe  
TITLE OF INVENTION: An Altered Major Histocompatibility  
TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the  
NUMBER OF SEQUENCES: 127  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
ZIP: 20005-3315

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,905  
FILING DATE: 07-JUNE-1995  
CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,818  
FILING DATE: 05-DEC-1991  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,473  
FILING DATE: 15-NOV-1991  
CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:  
NAME: Potter, Jane E. R.  
REGISTRATION NUMBER: 33,332  
REFERENCE/DOCKET NUMBER: 03495.0106-03000  
TELEPHONE: 202-408-4400  
TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 289 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

## US-08-484-905-79

Query Match 8.3%; Score 30; DB 2; Length 289;  
Best Local Similarity 100.0%; Pred. No. 2.9e-20;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 QDELVETRPAGDGTQKWAADVVPGEQ 276  
|||||

DB 226 QDELVETRPAGDGTQKWAADVVPGEQ 255  
|||||

## RESULT 13

US-08-481-985B-79  
Sequence 79, Application US/08481985B  
Patent No. 6011146

## GENERAL INFORMATION:

APPLICANT: Mottez, Estelle  
APPLICANT: Abastado, Jean-Pierre  
APPLICANT: Kourilsky, Philippe  
TITLE OF INVENTION: Altered Major Histocompatibility Complex  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
ADDRESSEE: Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
ZIP: 20005-3315

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/481,985B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/801,818  
FILING DATE: 05-DEC-1991  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/792,473  
FILING DATE: 15-NOV-1991  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Kenneth J.  
REGISTRATION NUMBER: 25,146  
REFERENCE/DOCKET NUMBER: 03495.0106-04000  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 289 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

## US-08-481-985B-79

Query Match 8.3%; Score 30; DB 3; Length 289;  
Best Local Similarity 100.0%; Pred. No. 2.9e-20;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 QDELVETRPAGDGTQKWAADVVPGEQ 276  
|||||

DB 226 QDELVETRPAGDGTQKWAADVVPGEQ 255  
|||||

## RESULT 14

US-08-370-476-79  
Sequence 79, Application US/08370476  
Patent No. 6153408

## GENERAL INFORMATION:

APPLICANT: Mottez, Estelle  
APPLICANT: Abastado, Jean-Pierre  
APPLICANT: Kourilsky, Philippe  
APPLICANT: Lone, Yu-Chun  
APPLICANT: Ogius, David  
APPLICANT: Casrouge, Armanda  
TITLE OF INVENTION: Altered Major Histocompatibility Complex

;; TITLE OF INVENTION:  
;; NUMBER OF SEQUENCES: 127  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
;; ADDRESSEE: Dunner  
;; STREET: 1300 I Street, N.W., Suite 700  
;; CITY: Washington  
;; STATE: D.C.  
;; ZIP: 20005-3315  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/370,476  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/117,575  
;; FILING DATE: 07-SEP-1993  
;; APPLICATION NUMBER: US 08/072,787  
;; FILING DATE: 06-JUN-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/801,818  
;; FILING DATE: 05-DEC-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/792,473  
;; FILING DATE: 15-NOV-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Meyers, Kenneth J.  
;; REGISTRATION NUMBER: 25,146  
;; REFERENCE/DOCKET NUMBER: 05243.0001-01000  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-408-4000  
;; TELEFAX: 202-408-4400  
;; INFORMATION FOR SEQ ID NO: 79:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 289 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; US-08-370-476-79

Query Match 8.3%; Score 30; DB 3; Length 289;  
Best Local Similarity 100.0%; Pred. No. 2.9e-20;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 QDTELVELTRPAGDGTFOKWAAVVPSGERQ 276  
|||  
Db 226 QDTELVELTRPAGDGTFOKWAAVVPSGERQ 255

RESULT 15  
US-08-484-905-105  
; Sequence 105, Application US/08484905  
; Patent No. 5976551  
; GENERAL INFORMATION:  
; APPLICANT: Mottez, Estelle  
; APPLICANT: Abastado, Jean-Pierre  
; APPLICANT: Kourilsky, Philippe  
; TITLE OF INVENTION: An Altered Major Histocompatibility  
; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the  
; NUMBER OF SEQUENCES: 127  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESS: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy Disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/484,905  
;; FILING DATE: 07-JUNE-1995  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/801,818  
;; FILING DATE: 05-DEC-1991  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/792,473  
;; FILING DATE: 15-NOV-1991  
;; CLASSIFICATION: 530  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Potter, Jane E. R.  
;; REGISTRATION NUMBER: 33,332  
;; REFERENCE/DOCKET NUMBER: 03495.0106-03000  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-408-4000  
;; TELEFAX: 202-408-4400  
;; INFORMATION FOR SEQ ID NO: 105:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 274 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; US-08-484-905-105

Query Match 8.0%; Score 29; DB 2; Length 274;  
Best Local Similarity 100.0%; Pred. No. 2.5e-19;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QDTELVELTRPAGDGTFOKWAAVVPSG 273  
|||  
Db 224 QDTELVELTRPAGDGTFOKWAAVVPSG 252

Search completed: July 13, 2005, 09:24:23  
Job time : 44 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 09:14:49 ; Search time 163 Seconds  
(without alignments)  
857.989 Million cell updates/sec

Title: US-09-819-371-4  
Perfect score: 362  
Sequence: 1 MAPRSLLLSGALALTDW.....QAQVTSAGSGVSLTANKV 362

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 1726220 seqs, 386332138 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 1726220

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

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17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*  
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22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	362	100.0	362	11 US-09-819-371-4	Sequence 4, Appli
2	261	72.1	362	15 US-10-257-021-82	Sequence 82, Appl
3	244	67.4	442	16 US-10-408-765A-1887	Sequence 1887, Ap
4	196	54.1	271	9 US-09-925-301-1431	Sequence 1431, Ap
5	175	48.3	274	11 US-09-819-371-5	Sequence 5, Appli
6	95	26.2	215	11 US-09-819-371-6	Sequence 6, Appli
7	70	19.3	186	15 US-10-264-049-4063	Sequence 4063, Ap
8	68	18.8	96	14 US-10-029-386-30718	Sequence 30718, Ap
9	44	12.2	77	14 US-10-029-386-34273	Sequence 34273, A
10	44	12.2	91	14 US-10-029-386-31089	Sequence 31089, A
11	44	12.2	104	9 US-09-925-302-835	Sequence 835, App

12	44	12.2	104	10 US-09-925-302-835	Sequence 835, App
13	44	12.2	365	17 US-10-741-600-941	Sequence 941, App
14	43	11.9	476	16 US-10-430-984-16	Sequence 16, Appl
15	43	11.9	500	16 US-10-430-984-15	Sequence 15, Appl
16	40	11.0	78	14 US-10-029-386-30752	Sequence 30752, A
17	40	11.0	371	15 US-10-085-198-72	Sequence 72, Appl
18	40	11.0	371	15 US-10-210-172-156	Sequence 156, App
19	39	10.8	91	9 US-09-864-761-38005	Sequence 38005, A
20	39	10.8	92	15 US-10-380-880-5	Sequence 5, Appli
21	39	10.8	169	16 US-10-741-601-383	Sequence 383, App
22	39	10.8	169	17 US-10-741-600-1135	Sequence 1135, Ap
23	39	10.8	198	16 US-10-741-601-387	Sequence 387, App
24	39	10.8	198	17 US-10-741-600-1143	Sequence 1143, Ap
25	39	10.8	224	15 US-10-380-880-8	Sequence 8, Appli
26	39	10.8	251	16 US-10-741-601-384	Sequence 384, App
27	39	10.8	251	17 US-10-741-600-1142	Sequence 1142, Ap
28	39	10.8	284	15 US-10-104-047-3648	Sequence 3648, Ap
29	39	10.8	326	15 US-10-380-880-7	Sequence 7, Appli
30	39	10.8	338	16 US-10-741-601-380	Sequence 380, App
31	39	10.8	338	16 US-10-741-601-388	Sequence 388, App
32	39	10.8	338	17 US-10-741-600-1134	Sequence 1134, Ap
33	39	10.8	338	17 US-10-741-600-1138	Sequence 1138, Ap
34	39	10.8	338	17 US-10-482-029-110	Sequence 110, App
35	39	10.8	343	16 US-10-741-601-379	Sequence 379, App
36	39	10.8	343	17 US-10-741-600-1139	Sequence 1139, Ap
37	39	10.8	379	15 US-10-093-463-78	Sequence 78, Appl
38	39	10.8	379	15 US-10-210-172-160	Sequence 160, App
39	38	10.5	145	9 US-09-810-560-8	Sequence 8, Appli
40	36	9.9	45	14 US-10-029-386-28883	Sequence 28883, A
41	32	8.8	91	9 US-09-864-761-35461	Sequence 35461, A
42	32	8.8	110	9 US-09-796-692-799	Sequence 799, App
43	32	8.8	110	9 US-09-796-692-2139	Sequence 2139, Ap
44	32	8.8	110	14 US-10-040-862-799	Sequence 799, App
45	32	8.8	110	14 US-10-040-862-2139	Sequence 2139, Ap

ALIGNMENTS

RESULT 1

US-09-819-371-4  
; Sequence 4, Application US/09819371  
; Publication No. US2004005344A1  
; GENERAL INFORMATION:  
; APPLICANT: Egawa, Kohji  
; TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can  
; TITLE OF INVENTION: Using Thereof  
; FILE REFERENCE: 30815  
; CURRENT APPLICATION NUMBER: US/09/819,371  
; CURRENT FILING DATE: 2002-03-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 362  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-819-371-4

Query Match	100.0%	Score 362;	DB 11;	Length 362;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 362;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MAPRSLLLSGALALTDWAGSHSLRYFSTAVSRGPRGEPRYIAVEYVDDTQFLRPSD	60	
Db	1	MAPRSLLLSGALALTDWAGSHSLRYFSTAVSRGPRGEPRYIAVEYVDDTQFLRPSD	60	
QY	61	AAIPRMEPRPVEGEGYQWTTGYAKANAQTRVALNLLRRYNQSEAGSHTLQGN	120	
Db	61	AAIPRMEPRPVEGEGYQWTTGYAKANAQTRVALNLLRRYNQSEAGSHTLQGN	120	
QY	121	GCDMGDCGLLRGYHQHAYDGDYISLNEDLSWTAADTVAQITQRFYAEAEFEFRY	180	
Db	121	GCDMGDCGLLRGYHQHAYDGDYISLNEDLSWTAADTVAQITQRFYAEAEFEFRY	180	

QY 181 LECELELLRRYLENGLETQADPPKAAVVAHPHPSDHEATLRCWALGFYPAEITLTWQR 240  
Db |||||  
QY 241 DGEETQDTLVELVETRPAGDGTQKAAVVPVSGEQRVYCHVQHEGLPQLILRWEQSPQ 300  
Db |||||  
QY 301 PTPIVIGIVAGLVVLGAVVTGAVVAAMVRKSSDRNRGSYSQAAVTDQAQSGVSLTAN 360  
Db |||||  
QY 361 KV 362  
Db |||||

*Auto-mated*

RESULT 2  
US-10-257-021-82  
; Sequence 82, Application US/10257021  
; Publication No. US20030211498A1  
; GENERAL INFORMATION:  
; APPLICANT: Morin, Patrice J.  
; APPLICANT: Sherman-Baust, Cheryl A.  
; APPLICANT: Pizer, Ellen S.  
; APPLICANT: Hough, Colleen D.  
; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER  
; FILE REFERENCE: 14014.036902  
; CURRENT APPLICATION NUMBER: US/10/257,021  
; CURRENT FILING DATE: 2002-10-03  
; PRIOR APPLICATION NUMBER: PCT/US01/10947  
; PRIOR FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: 60/194,336  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 82  
; LENGTH: 362  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-257-021-82

Query Match 72.1%; Score 261; DB 15; Length 362;  
Best Local Similarity 99.7%; Pred. No. 1e-233;  
Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MAPRSLLLLSGALALTDTWAGSHSLRYSTAVSRPGRGEPYIAVEYVDDTQFLRFSD 60  
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QY 61 AAPRMEPREPWEQEGPQYWEWTTGYAKANAQTDVALRNLLRRYNQSEAGSHTLQGMN 120  
Db |||||  
QY 121 GCDMGPDGRLRGYHQAHDGKDYISLNEEDLSRWSAATDTVAQITQRFYEAEEYAEFFRY 180  
Db |||||

QY 181 LECELELLRRYLENGLETQADPPKAAVVAHPHPSDHEATLRCWALGFYPAEITLTWQR 240  
Db |||||  
QY 241 DGEETQDTLVELVETRPAGDGTQKAAVVPVSGEQRVYCHVQHEGLPQLILRWEQSPQ 300  
Db |||||  
QY 301 PTPIVIGIVAGLVVLGAVVTGAVVAAMVRKSSDRNRGSYSQAAVTDQAQSGVSLTAN 360  
Db |||||

QY 361 KV 362  
Db |||||

Db 361 KV 362  
RESULT 3  
US-10-408-765A-1887  
; Sequence 1887, Application US/10408765A  
; Publication No. US20040101874A1  
; GENERAL INFORMATION:  
; APPLICANT: Ghosh, Soumitra S.  
; APPLICANT: Faby, Boin D.  
; APPLICANT: Zhang, Bing  
; APPLICANT: Gibson, Bradford W.  
; APPLICANT: Taylor, Steven W.  
; APPLICANT: Glenn, Gary M.  
; APPLICANT: Warnock, Dale E.  
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
; FILE REFERENCE: 660088.465  
; CURRENT APPLICATION NUMBER: US/10/408,765A  
; CURRENT FILING DATE: 2003-04-04  
; NUMBER OF SEQ ID NOS: 3077  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1887  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-408-765A-1887  
Query Match 67.4%; Score 244; DB 16; Length 442;  
Best Local Similarity 99.7%; Pred. No. 7.6e-218;  
Matches 344; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Db |||||  
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Db |||||  
QY 121 GCDMGPDGRLRGYHQAHDGKDYISLNEEDLSRWSAATDTVAQITQRFYEAEEYAEFFRY 180  
Db |||||  
QY 181 LECELELLRRYLENGLETQADPPKAAVVAHPHPSDHEATLRCWALGFYPAEITLTWQR 240  
Db |||||  
QY 241 DGEETQDTLVELVETRPAGDGTQKAAVVPVSGEQRVYCHVQHEGLPQLILRWEQSPQ 300  
Db |||||  
QY 301 PTPIVIGIVAGLVVLGAVVTGAVVAAMVRKSSDRNRGSYSQAA 345  
Db |||||

RESULT 4  
US-09-925-301-1431  
; Sequence 1431, Application US/09925301  
; Patent No. US20020052308A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA106  
; CURRENT APPLICATION NUMBER: US/09/925,301  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05882  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1694  
; SOFTWARE: Patentin Ver. 2.0

*Page 2 of 8*



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; SEQ ID NO 1431
; LENGTH: 271
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1431

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Query Match	54.1%	Score 196;	DB 9;	Length 271;
Best Local Similarity	100.0%;	Pred. No. 2e-173;		
Matches 196;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MAPRSLLLLSGALALTDTWAGSHSLRYFSTAVSRPGCEPRYIAVEYVDDTQFLRFPDSD	60	
Db	7	MAPRSLLLLSGALALTDTWAGSHSLRYFSTAVSRPGCEPRYIAVEYVDDTQFLRFPDSD	66	
Qy	61	AAIPRMPREPWPVEQGPQYEWTTGYAKANAQTDRLVALRNLRRYNOSEAGSHTLQGMN	120	
Db	67	AAIPRMPREPWPVEQGPQYEWTTGYAKANAQTDRLVALRNLRRYNOSEAGSHTLQGMN	126	
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Db	127	GCDMPGGRLLRGVQHAYDCKDYISLNEDLRSTAAADTVQAQITQRFYAEAYAEFPRTY	186	
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## RESULT 5

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US-09-819-371-5
; Sequence 5, Application US/09819371
; Publication No. US20040053344A1
GENERAL INFORMATION:
APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Sp
; TITLE OF INVENTION: Using Thereof
; FILE REFERENCE: 30815
CURRENT APPLICATION NUMBER: US/09/
CURRENT FILING DATE: 2002-03-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 274
TYPE: PRT
ORGANISM: Homo sapiens
US-09-819-371-5

```

Query Match	48.3%	Score 175;	DB 11;	Length 274;
Best Local Similarity	100.0%;	Prod. No. 6.6e-154;		
Matches 175;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	22	GSHSLRYFSTAVSPGRGEPYIAVEYVDDTQFLRFSDAAI	PRMEPREPWVEQGPYW	81
Db	1	GSHSLRYFSTAVSPGRGEPYIAVEYVDDTQFLRFSDAAI	PRMEPREPWVEQGPYW	60
Qy	82	EWTGTGAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHOHYDVG	141	
Db	61	EWTGTGAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHOHYDVG	120	
Qy	142	KDYISLNEDLRSWTAADTVAQITQRFYEAEYAEFFTYLGECELELLRRYLENG	196	
Db	121	KDYISLNEDLRSWTAADTVAQITQRFYEAEYAEFFTYLGECELELLRRYLENG	175	

## RESULT 6

```

US-09-819-371-6
; Sequence 6, Application US/09819371
; Publication No. US20040053344A1
; GENERAL INFORMATION:
; APPLICANT: Egawa, Kohji
; TITLE OF INVENTION: Cancer Cell-Sp.
; TITLE OF INVENTION: Using Thereof
; FILE REFERENCE: 30815
; CURRENT APPLICATION NUMBER: US/09/

```

```

; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-819-371-6

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Query Match	26.2%	Score 95;	DB 11;	Length 215;
Best Local Similarity	100.0%;	Pred. No. 1.2e-79;		
Matches 95;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	44	IAVEYVDDTQFLRFDSDAIPRMEPREPVMVEQGQPYWEMTTGYAKANAQTDRAVALNLL	103	
Db	1	IAVEYVDDTQFLRFDSDAIPRMEPREPVMVEQGQPYWEMTTGYAKANAQTDRAVALNLL	60	
Qy	104	RRYNQSEAGSHITLQMGNGCDMGDPDGLLRGYHOHA	138	
Db	61	RRYNQSEAGSHITLQMGNGCDMGDPDGLLRGYHOHA	95	

## RESULT 7

```

US-10-264-049-4063
; Sequence 4063, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4063
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (76)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (77)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (86)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (107)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (123)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (124)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (136)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (148)

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OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: MISC\_FEATURE  
LOCATION: (163}  
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: MISC\_FEATURE  
LOCATION: (174}  
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: MISC\_FEATURE  
LOCATION: (175}  
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: MISC\_FEATURE  
LOCATION: (176}  
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: MISC\_FEATURE  
LOCATION: (180}  
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
US-10-264-049-4063

Query Match 19.3%; Score 70; DB 15; Length 186;  
Best Local Similarity 100.0%; Pred. No. 1.7e-56;  
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 YAKANAQTRVALNRLRRYNQSEAGSHTLQMGNGCDMGPDGRLLRGVHGHAYDGDYIS 146  
|||||  
Db 1 YAKANAQTRVALNRLRRYNQSEAGSHTLQMGNGCDMGPDGRLLRGVHGHAYDGDYIS 60  
|||||

QY 147 LNEDLRSWTA 156  
|||||  
Db 61 LNEDLRSWTA 70  
|||||

## RESULT 8

US-10-029-386-30718  
Sequence 30718, Application US/10029386  
Publication No. US20030194704A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Rank, David R.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: AEOMICA-X-2  
CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 30718  
LENGTH: 96  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO CHR6.1  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12  
OTHER INFORMATION: SWISSPROT HIT: P30511, EVALUE 2.00e-52  
US-10-029-386-30718

Query Match 18.8%; Score 68; DB 14; Length 96;  
Best Local Similarity 100.0%; Pred. No. 7e-55;  
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 204 DPPKAHVHHPISDHEATRCWALGFYPAEITLTWQDGEQQTDELVETRPAGDGTQ 263  
|||||  
Db 2 DPPKAHVHHPISDHEATRCWALGFYPAEITLTWQDGEQQTDELVETRPAGDGTQ 61  
|||||

QY 264 KWAAVVVP 271  
|||||  
Db 62 KWAAVVVP 69  
|||||

## RESULT 9

US-10-029-386-34273  
Sequence 34273, Application US/10029386  
Publication No. US20030194704A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Rank, David R.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: AEOMICA-X-2  
CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 34273  
LENGTH: 77  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO CHR6.1  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 53  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.4  
OTHER INFORMATION: SWISSPROT HIT: P30507, EVALUE 6.00e-42  
US-10-029-386-34273

Query Match 12.2%; Score 44; DB 14; Length 77;  
Best Local Similarity 100.0%; Pred. No. 1.2e-32;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLVELTRPAGDGTQKWAAVVVPSEGEQRYTCHVQHEGLP 288  
|||||  
Db 25 QTQDTLVELTRPAGDGTQKWAAVVVPSEGEQRYTCHVQHEGLP 68  
|||||

## RESULT 10

US-10-029-386-31089  
Sequence 31089, Application US/10029386  
Publication No. US20030194704A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Rank, David R.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: AEOMICA-X-2  
CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 31089  
LENGTH: 91  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC004204.1  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1  
OTHER INFORMATION: SWISSPROT HIT: P30509, EVALUE 1.00e-52  
US-10-029-386-31089

Query Match 12.2%; Score 44; DB 14; Length 91;  
Best Local Similarity 100.0%; Pred. No. 1.3e-32;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLVELTRPAGDGTQKWAAVVVPSEGEQRYTCHVQHEGLP 288  
|||||  
Db 41 QTQDTLVELTRPAGDGTQKWAAVVVPSEGEQRYTCHVQHEGLP 84  
|||||

```
RESULT 11
US-09-925-302-835
; Sequence 835, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 835
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (95)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-835

Query Match      12.2%; Score 44; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.5e-32;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLTVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 288
Db 32 QTQDTLTVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 75

RESULT 12
US-09-925-302-835
; Sequence 835, Application US/09925302
; Patent No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 835
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (95)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-835

Query Match      12.2%; Score 44; DB 10; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.5e-32;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLTVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 288
Db 32 QTQDTLTVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 75

RESULT 13
US-10-741-600-941
```

```
; Sequence 941, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 941
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-941

Query Match      12.2%; Score 44; DB 17; Length 365;
Best Local Similarity 100.0%; Pred. No. 4.6e-32;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 QTQDTLTVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 288
Db 248 QTQDTLTVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 291

RESULT 14
US-10-430-984-16
; Sequence 16, Application US/10430984
; Publication No. US20040225112A1
; GENERAL INFORMATION:
; APPLICANT: The Board of Trustees of the University of Arkansas
; APPLICANT: Crew, Mark D
; TITLE OF INVENTION: Genes Encoding Single Chain Human Leukocyte Antigen E (HLA-E)
; FILE REFERENCE: Proteins to Prevent Natural Killer Cell-Mediated Cytotoxicity
; CURRENT APPLICATION NUMBER: US/10/430,984
; CURRENT FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 476
; TYPE: PRT
; ORGANISM: human leukocyte antigen E-Single chain dimer
US-10-430-984-16

Query Match      11.9%; Score 43; DB 16; Length 476;
Best Local Similarity 100.0%; Pred. No. 5e-31;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 246 TQDTLTVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 288
Db 364 TQDTLTVETRPAGDGTGFKWAAVVVPSGEEQRYTCHVQHEGLP 406

RESULT 15
US-10-430-984-15
; Sequence 15, Application US/10430984
; Publication No. US20040225112A1
; GENERAL INFORMATION:
; APPLICANT: The Board of Trustees of the University of Arkansas
; APPLICANT: Crew, Mark D
; TITLE OF INVENTION: Genes Encoding Single Chain Human Leukocyte Antigen E (HLA-E)
; FILE REFERENCE: Proteins to Prevent Natural Killer Cell-Mediated Cytotoxicity
; CURRENT APPLICATION NUMBER: US/10/430,984
; CURRENT FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 500
; TYPE: PRT
; ORGANISM: human leukocyte antigen E-Single chain Trimer
```

```
Query Match 11.9%; Score 43; DB 16; Length 500;
Best Local Similarity 100.0%; Pred. No. 5.2e-31;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	246	TQDT	VTET	TR	PAGD	GT	TF	KWAA	VV	VP	SGEE	QRYT	CHVQ	HEGL	P	288
Db	388	TQDT	VTET	TR	PAGD	GT	TF	KWAA	VV	VP	SGEE	QRYT	CHVQ	HEGL	P	430

Search completed: July 13, 2005, 09:28:24  
Job time : 164 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 08:59:16 ; Search time 164 Seconds  
(without alignments)  
853.703 Million cell updates/sec

Title: US-09-819-371-4

Perfect score: 362

Sequence: 1 MAPRSLLLSGALATDTW.....QAAVTDSAGSGVSLTANKV 362

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A Geneseq\_16Dec04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	261	72.1	362	4	AAG64617 Human can
2	261	72.1	362	4	ABBS0296 HLA-Cw ov
3	261	72.1	362	7	ADFS5587 Human can
4	261	72.1	362	8	ADJ75372 Marker ge
5	261	72.1	362	8	ADP12500 Protein e
6	261	72.1	362	8	ABM80784 Tumour-as
7	261	72.1	362	8	ADP23768 PRO polyp
8	261	72.1	362	8	ADP23768 PRO polyp
9	244	67.4	442	7	ADJ70081 Human can
10	196	54.1	271	3	ABBS0296 Human can
11	196	54.1	677	4	ABBS0296 Human can
12	175	48.3	274	4	AAG64618 Human can
13	175	48.3	274	7	ADFS5588 Fragment
14	153	42.3	215	4	AAG64619 Human can
15	153	42.3	215	7	ADFS5589 Fragment
16	148	40.9	349	8	ADQ55964 Novel hum
17	120	33.1	120	3	AAG00209 Human sec
18	74	20.4	120	7	ADJ12106 Novel hum
19	70	19.3	186	5	ABP42931 Human ova
20	68	18.8	96	8	ABBS07084 Human gen
21	44	12.2	77	8	ABBS06039 Human gen
22	44	12.2	91	8	ABBS07455 Human gen
23	44	12.2	104	3	ABBS04997 Lung can
24	44	12.2	274	1	AAP80911 Consensus
25	44	12.2	365	8	ADP12521 Protein e

26	44	12.2	365	8	ADQ39278	Adq39278 Human myo
27	44	12.2	366	2	AAR12466	Aar12466 HLA-C exo
28	44	12.2	366	2	AAY07033	Aay07033 Breast ca
29	44	12.2	366	7	ADI62997	Adi62997 Human apo
30	44	12.2	366	7	ADP65326	Adp65326 Human HLA
31	44	12.2	366	7	ADP65316	Adp65316 Human hla
32	44	12.2	366	8	ADP74305	Adp74305 PRO polyp
33	44	12.2	371	8	ADS10818	Ads10818 Human the
34	44	12.2	374	4	AAO13073	Aao13073 Human pol
35	44	12.2	380	4	AAU32883	Aau32883 Novel hum
36	43	11.9	120	4	AAB90793	Aab90793 Human she
37	43	11.9	130	5	ADI80341	Adi80341 Human leu
38	43	11.9	358	8	ABM80782	Abm80782 Tumour-as
39	43	11.9	358	8	ADP23060	Adp23060 PRO polyp
40	43	11.9	362	7	ADE31177	Ade31177 Human dia
41	40	11.0	78	8	ABO57118	Abo57118 Human gen
42	40	11.0	187	8	ADP29434	Adp29434 Human sec
43	40	11.0	314	8	ADF69311	Adf69311 Human lun
44	40	11.0	371	5	ADH48788	Adh48788 NOV31 pro
45	40	11.0	371	7	ADE40250	Ade40250 Human NOV

ALIGNMENTS

RESULT 1  
AAG64617  
ID AAG64617 standard; protein; 362 AA.

AC AAG64617;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Human cancer cell specific HLA-F antigen SEQ ID 4.  
XX  
KW HLA-F antigen; cancer cell specific; human.

OS Homo sapiens.  
XX  
PN JP2001095584-A.  
XX  
PD 10-APR-2001.  
XX  
PF 30-SEP-1999; 99JP-00279566.  
XX  
PR 30-SEP-1999; 99JP-00279566.

XX (EGAW/) EGAWA K.  
PA (MEDI-) MEDINET KK.  
PA (KIMU/) KIMURA K.  
DR WPI; 2001-360493/38.  
DR N-PSDB; AAH45555.

XX Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.  
PS Disclosure; Page 9-10; 12pp; Japanese.

CC This invention relates to a cancer cell specific HLA-F antigen. The  
CC invention includes DNA encoding the antigen, and a method for the  
CC preparation of the cancer cell specific HLA-F antigen. The antigen may be  
CC used in a method to diagnose cancer, in which the protein is used to  
CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present  
CC sequence represents the cancer cell-specific HLA-F antigen of the  
CC invention

XX Sequence 362 AA;

Query Match 72.1%; Score 261; DB 4; Length 362;  
Best Local Similarity 99.7%; Pred. No. 1.4e-229;  
Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MAPRSLLLSGALATDTWAGSHSLRYSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSD 60

Db 1 MAPRSLLLLSGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIAYVEYVDDTQFLRFDS 60  
 Qy 61 AAI PRMEPREPWEQEGPOYWEWTTGYAKANAQTDVALNLLRRYVNSQAGSHTLQGNW 120  
 Db 61 AAI PRMEPREPWEQEGPOYWEWTTGYAKANAQTDVALNLLRRYVNSQAGSHTLQGNW 120  
 Qy 121 GCDMGPDGRLRGYHQHAYDGDYISLNEDLSRWSAADTVAQITQRFYEAEYAEFEFTY 180  
 Db 121 GCDMGPDGRLRGYHQHAYDGDYISLNEDLSRWSAADTVAQITQRFYEAEYAEFEFTY 180  
 Qy 181 LEGECLELLRRYLENGLETQORADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQR 240  
 Db 181 LEGECLELLRRYLENGLETQORADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQR 240  
 Qy 241 DGEEOQTDELVELTRPAGDGTQKAAVVPVSGEORYTCHVQHEGLPQLILRWEQSPQ 300  
 Db 241 DGEEOQTDELVELTRPAGDGTQKAAVVPVSGEORYTCHVQHEGLPQLILRWEQSPQ 300  
 Qy 301 PTPIVIGIVAGLVVLGAVVTGAVVAAMVRKSSDRNRGSYSQAAVTDQAQSGSVSLTAN 360  
 Db 301 PTPIVIGIVAGLVVLGAVVTGAVVAAMVRKSSDRNRGSYSQAAVTDQAQSGSVSLTAN 360  
 Qy 361 KV 362  
 Db 361 KV 362

## RESULT 2

ABB50296  
 ID ABB50296 standard; protein; 362 AA.

AC ABB50296;

DT 08-FEB-2002 (first entry)

DE HLA-Cw ovarian tumour marker protein, SEQ ID NO:82.

XX Ovarian tumour marker gene; human; overexpression; upregulation;  
 KW epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;  
 KW identification; serous cystadenoma; borderline serous tumour;  
 KW serous cystadenocarcinoma; mucinous cystadenocarcinoma;  
 KW mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma;  
 KW undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma;  
 KW adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE;  
 KW immune response pathway; cell proliferation regulation; protein folding;  
 KW membrane localised; secreted; therapeutic target; cytostatic;  
 KW gene therapy; vaccine.

XX Homo sapiens.

OS WO200175177-A2.

PN 11-OCT-2001.

XX 03-APR-2001; 2001WO-US010947.

XX 03-APR-2000; 2000US-0194336P.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PA Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;

XX WPI: 2001-626450/72.

DR N-PSDB; ABA83122.

XX Detecting and identifying ovarian tumor, identifying increased risk for  
 PT developing ovarian cancer, and determining effectiveness of ovarian  
 PT cancer treatment, by measuring expression level of ovarian tumor marker  
 PT gene.

XX Claim 23; Page 126-127; 140pp; English.

PS XX

CC The invention relates to methods for diagnosing and prognosing ovarian  
 CC tumours in an individual via the detection and measurement of the  
 CC expression of ovarian tumour marker genes (ABA83081-ABA83122, ABA83180,  
 CC ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179,  
 CC ABA83181 and ABA83183). The methods of the invention are useful for  
 CC detecting an ovarian tumour in a patient, for identifying an individual  
 CC at increased risk for developing ovarian cancer, in prognostic tests for  
 CC assessing the relative severity of ovarian cancer, in tests for  
 CC monitoring a patient in remission from ovarian cancer and in tests for  
 CC monitoring disease status in a patient being treated for ovarian cancer.  
 CC The methods can additionally be used to identify a particular tumour as  
 CC being an ovarian tumour (i.e., an epithelial ovarian tumour selected from  
 CC serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma,  
 CC mucinous cystadenoma, borderline mucinous tumour, mucinous  
 CC cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma,  
 CC clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner  
 CC tumour. The ovarian tumour marker genes of the invention were identified  
 CC using SAGE (serial analysis of gene expression) and were found to be  
 CC overexpressed in a broad variety of ovarian epithelial tumour cells  
 CC relative to normal ovarian epithelial cells. The marker genes are  
 CC implicated in immune response pathways, in the regulation of cell  
 CC proliferation and in protein folding, and many of these are membrane-  
 CC localised or secreted. In addition to their use as diagnostic and  
 CC prognostic markers, the ovarian tumour marker genes of their encoded  
 CC proteins may be used as therapeutic targets for the treatment and  
 CC prevention of ovarian cancer. Sequences ABB50257-ABB50299 represent  
 CC proteins encoded by ovarian tumour marker genes of the invention  
 XX  
 SQ Sequence 362 AA;

Query Match 72.1%; Score 261; DB 4; Length 362;

Best Local Similarity 99.7%; Pred. No. 1.4e-229;

Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAPRSLLLLSGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIAYVEYVDDTQFLRFDS 60  
 Db 1 MAPRSLLLLSGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIAYVEYVDDTQFLRFDS 60  
 Qy 61 AAI PRMEPREPWEQEGPOYWEWTTGYAKANAQTDVALNLLRRYVNSQAGSHTLQGNW 120  
 Db 61 AAI PRMEPREPWEQEGPOYWEWTTGYAKANAQTDVALNLLRRYVNSQAGSHTLQGNW 120  
 Qy 121 GCDMGPDGRLRGYHQHAYDGDYISLNEDLSRWSAADTVAQITQRFYEAEYAEFEFTY 180  
 Db 121 GCDMGPDGRLRGYHQHAYDGDYISLNEDLSRWSAADTVAQITQRFYEAEYAEFEFTY 180  
 Qy 181 LEGECLELLRRYLENGLETQORADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQR 240  
 Db 181 LEGECLELLRRYLENGLETQORADPPKAHVAHPISDHEATLRCWALGFYPAEITLTWQR 240  
 Qy 241 DGEEOQTDELVELTRPAGDGTQKAAVVPVSGEORYTCHVQHEGLPQLILRWEQSPQ 300  
 Db 241 DGEEOQTDELVELTRPAGDGTQKAAVVPVSGEORYTCHVQHEGLPQLILRWEQSPQ 300  
 Qy 301 PTPIVIGIVAGLVVLGAVVTGAVVAAMVRKSSDRNRGSYSQAAVTDQAQSGSVSLTAN 360  
 Db 301 PTPIVIGIVAGLVVLGAVVTGAVVAAMVRKSSDRNRGSYSQAAVTDQAQSGSVSLTAN 360  
 Qy 361 KV 362  
 Db 361 KV 362

## RESULT 3

ADF55587

ID ADF55587 standard; protein; 362 AA.

XX ADF55587;

AC ADF55587;

XX 12-FEB-2004 (first entry)

XX Human cancer-cell specific HLA-F antigen.

KW Cancer; human leukocyte antigen-F; HLA-F;  
KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
KW major histocompatibility complex; MHC; cancer cell; human.  
OS Homo sapiens.  
XX JP2003012544-A.  
XX 15-JAN-2003.  
XX 27-MAR-2002; 2002JP-00088991.  
XX 27-MAR-2001; 2001JP-00090121.  
XX (EGAWA/) EGAWA K.  
XX (MEDI-) MEDINET KK.  
XX (KIMU/) KIMURA Y.  
XX WPI; 2003-486263/46.  
XX N-PSDB; ADF5584.  
XX Agent for preventing and treating cancer, comprising human leukocyte  
XX antigen-F DNA, or a plasmid or viral vector comprising the DNA.  
XX Claim 5; SEQ ID NO 4; 19pp; Japanese.  
XX The present invention relates to an agent for preventing or treating  
XX cancer. The agent comprises a portion or a complete sequence of a human  
XX leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of  
XX presenting a cancer-cell specific antigen transformed with HLA-F DNA, or  
XX a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte  
XX (CTL) inducer which induces CTL which is non-specific to an organ, is  
XX unrestricted to the major histocompatibility complex (MHC) and specific  
XX to a cancer cell, and an anti-HLA-F antibody. The agent of the invention  
XX is useful for treating or preventing cancer. A cell capable of presenting  
XX a cancer-cell specific antigen is useful for measuring HLA-F antigen and  
XX for diagnosing cancer. The present sequence represents human cancer-cell  
XX specific HLA-F antigen.  
XX Sequence 362 AA;  
Query Match 72.1%; Score 261; DB 7; Length 362;  
Best Local Similarity 99.7%; Pred. No. 1.4e-229;  
Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MAPRSLLLLSGALALTDTWAGSHSLRYFSTAVSRPGRGPRYIAVEYVDVDTQFLRFDSD 60  
DB 1 MAPRSLLLLSGALALTDTWAGSHSLRYFSTAVSRPGRGPRYIAVEYVDVDTQFLRFDSD 60  
QY 61 AAIPRMEPREPWVEQEGPOQWETTGAKANAQTDVRLNLLRRYNQSEAGSHTLQGMN 120  
DB 61 AAIPRMEPREPWVEQEGPOQWETTGAKANAQTDVRLNLLRRYNQSEAGSHTLQGMN 120  
QY 121 GCDMGDPDGRLLRGYHQAIDYKDYISLNEDLRSWTAADTVAQITQRFYAEAEYAEFRTY 180  
DB 121 GCDMGDPDGRLLRGYHQAIDYKDYISLNEDLRSWTAADTVAQITQRFYAEAEYAEFRTY 180  
QY 181 LEGECLELLRRLYLENGLETQRPKAVHAHPISDHEATLRCWALGFVPAEITLWQR 240  
DB 181 LEGECLELLRRLYLENGLETQRPKAVHAHPISDHEATLRCWALGFVPAEITLWQR 240  
QY 241 DGESEQTDTELVTETPAGDGTFOKAAVVPSEGEQRYTCHVQHEGLPQPLILRLWQSPQ 300  
DB 241 DGESEQTDTELVTETPAGDGTFOKAAVVPSEGEQRYTCHVQHEGLPQPLILRLWQSPQ 300  
QY 301 PTPIVIGIVAGLVVLGAVVTGAVVAAVMWRKSSDRNRGYSQAAVTDSAQSGVSLTAN 360  
DB 301 PTPIVIGIVAGLVVLGAVVTGAVVAAVMWRKSSDRNRGYSQAAVTDSAQSGVSLTAN 360  
QY 361 KV 362  
DB 361 KV 362

RESULT 4  
ADJ75372  
ID ADJ75372 standard; protein; 362 AA.  
XX  
XX AC ADJ75372;  
XX  
XX DT 20-MAY-2004 (first entry)  
XX  
XX DE Marker gene related amino acid sequence SEQ ID NO:624.  
XX  
XX KW bronchial asthma; chronic obstructive pulmonary disease;  
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;  
KW gene therapy; marker.  
XX  
XX OS Homo sapiens.  
XX  
XX PN EP1394274-A2.  
XX  
XX PD 03-MAR-2004.  
XX  
XX PF 04-AUG-2003; 2003EP-00254857.  
XX  
XX PR 06-AUG-2002; 2002JP-00229312.  
XX  
XX PS 20-MAR-2003; 2003JP-00077212.  
XX  
XX (GENO-) GENOX RES INC.  
XX  
XX PA Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;  
XX  
XX WPI; 2004-193155/19.  
XX  
XX Testing for bronchial asthma or chronic obstructive pulmonary disease by  
XX comparing the expression level of a marker gene in a biological sample  
XX from a subject with the expression level of the gene in a sample from a  
XX healthy subject.  
XX  
XX Example 11; SEQ ID NO 624; 241pp; English.  
XX  
XX The present invention describes a method of testing for bronchial asthma  
XX or chronic obstructive pulmonary disease. The method comprises  
XX determining the expression level of a marker gene in a biological sample  
XX from a subject, comparing the expression level determined with the  
XX expression level of the marker gene in a biological sample from a healthy  
XX subject, and judging whether the subject has bronchial asthma or chronic  
XX obstructive pulmonary disease. The marker gene comprises: (a) a group of  
XX genes (S1) whose expression levels increase when respiratory epithelial  
XX cells are stimulated with interleukin-13; or (b) a group of genes (S2)  
XX whose expression levels decrease when respiratory epithelial cells are  
XX stimulated with interleukin-13. Also described: (1) a reagent (I) for  
XX testing for bronchial asthma or chronic obstructive pulmonary disease;  
XX (2) a kit for screening for a candidate compound for a therapeutic agent  
XX to treat bronchial asthma or chronic obstructive pulmonary disease; (3)  
XX an animal model for bronchial asthma or chronic obstructive pulmonary  
XX disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a  
XX method for producing an animal model for bronchial asthma or chronic  
XX obstructive pulmonary disease; (6) a therapeutic agent for bronchial  
XX asthma or chronic obstructive pulmonary disease, comprising the compound,  
XX a marker gene or an antisense nucleic acid corresponding to a portion of  
XX the marker gene, a ribozyme, a polynucleotide that suppresses the  
XX expression of the gene through an RNAi effect or an antibody recognising  
XX a protein encoded by a marker gene; and (7) a DNA chip for testing for  
XX bronchial asthma or a chronic obstructive pulmonary disease, on which a  
XX probe has been immobilised to assay a marker gene. (I) has respiratory  
XX and antiasthmatic activities, and can be used in gene therapy. The method  
XX is useful for testing for or screening for a therapeutic agent for  
XX bronchial asthma or chronic obstructive pulmonary disease. The present  
XX sequence is used in the exemplification of the present invention.  
XX  
XX Sequence 362 AA;  
Query Match 72.1%; Score 261; DB 8; Length 362;  
Best Local Similarity 99.7%; Pred. No. 1.4e-229;

Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY 1 MAPRSLLLLSGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIAYEVYDDTQFLRFSD 60	
DB 1 MAPRSLLLLSGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIAYEVYDDTQFLRFSD 60	
QY 61 AAI PRMEPREPWEQEGPQYWEWTTGYAKANAQTDRLVALNLLRRYNOSEAGSHTLQGMN 120	
DB 61 AAI PRMEPREPWEQEGPQYWEWTTGYAKANAQTDRLVALNLLRRYNOSEAGSHTLQGMN 120	
QY 121 GCDMGPDGRLRGYHQHAYDGDYISLNEDLSWTAADTVAQITQRFYEAEEYAEFRY 180	
DB 121 GCDMGPDGRLRGYHQHAYDGDYISLNEDLSWTAADTVAQITQRFYEAEEYAEFRY 180	
QY 181 LECELELLRRYLENGLETQADPPKAHVAHPISDHEATLRCWALGYPAEITLTWQR 240	
DB 181 LECELELLRRYLENGLETQADPPKAHVAHPISDHEATLRCWALGYPAEITLTWQR 240	
QY 241 DGEEOQTDELVETRPAGDGTQKWAAVVVPSEGEQRYTCHVQHEGLPQPLILRWEQSPQ 300	
DB 241 DGEEOQTDELVETRPAGDGTQKWAAVVVPSEGEQRYTCHVQHEGLPQPLILRWEQSPQ 300	
QY 301 PTPIVIGIVAGLVVLGAVVTGAVVAAMVRKSSDRNRGSYSQAAVTDSAQSGVSLTAN 360	
DB 301 PTPIVIGIVAGLVVLGAVVTGAVVAAMVRKSSDRNRGSYSQAAVTDSAQSGVSLTAN 360	
QY 361 KV 362	
DB 361 KV 362	
RESULT 5	
ID ADP12500 standard; protein; 362 AA.	
XX AC ADP12500;	
XX 12-AUG-2004 (first entry)	
XX Protein encoded by mRNA of the invention #110.	
XX transplant rejection; immune system; rheumatoid arthritis; lupus;	
KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.	
XX Homo sapiens.	
XX WO2004042346-A2.	
XX 21-MAY-2004.	
XX 24-APR-2003; 2003WO-US012946.	
XX 24-APR-2002; 2002US-00131831.	
XX 20-DEC-2002; 2002US-00325899.	
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.	
XX Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;	
PI Rosenberg S;	
XX WPI; 2004-400724/37.	
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,	
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant	
PT rejection, in an individual, comprises detecting the expression level of	
PT the genes.	
XX Claim 65; SEQ ID NO 2509; 1762pp; English.	
XX The present invention relates to diagnosing or monitoring transplant	
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual	
CC comprises detecting the expression level of one or more genes. The	
CC methods, system and kits are useful in diagnosing or monitoring	

CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic	
CC islet, lung, bone marrow or stem cell transplant rejection,	
CC xenotransplant rejection or mechanical organ replacement rejection, in an	
CC individual. The method is also useful in assessing the immune status of	
CC an individual. The methods are also useful in diagnosing and monitoring	
CC diseases that involve the immune system, e.g. rheumatoid arthritis,	
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or	
CC viral, bacterial or fungal infection. The present sequence represents a	
XX protein that is encoded by the mRNA of the invention.	
SQ Sequence 362 AA;	
Query Match 72.1%; Score 261; DB 8; Length 362;	
Best Local Similarity 99.7%; Pred. No. 1.4e-229;	
Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY 1 MAPRSLLLLSGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIAYEVYDDTQFLRFSD 60	
DB 1 MAPRSLLLLSGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIAYEVYDDTQFLRFSD 60	
QY 61 AAI PRMEPREPWEQEGPQYWEWTTGYAKANAQTDRLVALNLLRRYNOSEAGSHTLQGMN 120	
DB 61 AAI PRMEPREPWEQEGPQYWEWTTGYAKANAQTDRLVALNLLRRYNOSEAGSHTLQGMN 120	
QY 121 GCDMGPDGRLRGYHQHAYDGDYISLNEDLSWTAADTVAQITQRFYEAEEYAEFRY 180	
DB 121 GCDMGPDGRLRGYHQHAYDGDYISLNEDLSWTAADTVAQITQRFYEAEEYAEFRY 180	
QY 181 LECELELLRRYLENGLETQADPPKAHVAHPISDHEATLRCWALGYPAEITLTWQR 240	
DB 181 LECELELLRRYLENGLETQADPPKAHVAHPISDHEATLRCWALGYPAEITLTWQR 240	
QY 241 DGEEOQTDELVETRPAGDGTQKWAAVVVPSEGEQRYTCHVQHEGLPQPLILRWEQSPQ 300	
DB 241 DGEEOQTDELVETRPAGDGTQKWAAVVVPSEGEQRYTCHVQHEGLPQPLILRWEQSPQ 300	
QY 301 PTPIVIGIVAGLVVLGAVVTGAVVAAMVRKSSDRNRGSYSQAAVTDSAQSGVSLTAN 360	
DB 301 PTPIVIGIVAGLVVLGAVVTGAVVAAMVRKSSDRNRGSYSQAAVTDSAQSGVSLTAN 360	
QY 361 KV 362	
DB 361 KV 362	
RESULT 6	
ABM80784	
ID ABM80784 standard; protein; 362 AA.	
XX AC ABM80784;	
XX 18-NOV-2004 (first entry)	
XX Tumour-associated antigenic target (TAT) polypeptide PRO81414, SEQ:2018.	
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;	
KW tumour; diagnosis; cell proliferative disorder; breast cancer;	
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;	
KW central nervous system cancer; bladder cancer; pancreatic cancer;	
KW cervical cancer; melanoma; leukaemia; hybridisation probe;	
KW chromosome identification; chromosome mapping; gene mapping;	
KW gene therapy; cytostatic.	
XX Homo sapiens.	
OS WO2004030615-A2.	
PN 15-APR-2004.	
XX 29-SEP-2003; 2003WO-US028547.	
XX 02-OCT-2002; 2002US-0414971P.	



PA (GETH ) GENENTECH INC.  
XX Wu TD, Zhang Z, Zhou Y;  
XX WPI; 2004-347921/32.  
DR N-PSDB; ACN38477.  
XX  
XX New tumor-associated antigenic target polypeptides and nucleic acids,  
PT useful in preparing a medicament for treating or detecting a  
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or  
PT prostate cancer or tumor.  
XX  
XX  
PS Claim 12; SEQ ID NO 2018; 7273pp; English.  
XX  
XX The invention relates to human tumour-associated antigenic target (TAT)  
CC polypeptides, and their related nucleic acids. The TAT polypeptides are  
CC overexpressed in cancer tissues compared to normal tissues, and may thus  
CC serve as effective targets for the diagnosis and treatment of cancer in  
CC mammals. The invention also relates to nucleic acid and polypeptide  
CC sequences at least 80% identical to the TAT nucleic acids and  
CC polypeptides; expression vectors and host cells comprising a TAT nucleic  
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic  
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a  
CC TAT polypeptide; and methods and compositions for the treatment or  
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,  
CC antibodies, antagonists, binding molecules and compositions are useful  
CC for diagnosing or treating a cell proliferative disorder associated with  
CC increased TAT expression, particularly cancers such as breast cancer,  
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder  
CC cancer, pancreatic cancer, cervical cancer, cancers of the central  
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be  
CC used as hybridisation probes, in chromosome and gene mapping, in  
CC chromosome identification and in gene therapy. The present sequence  
CC represents a TAT polypeptide of the invention  
XX  
SQ Sequence 362 AA;  
  
Query Match 72.1%; Score 261; DB 8; Length 362;  
Best Local Similarity 99.7%; Pred. No. 1.4e-229;  
Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 MAPRSLLLLSGALALTDWAGSHSLRYFSTAVSRGGRGPRYIAVEYVDDTQFLRPDSD 60  
Db 1 MAPRSLLLLSGALALTDWAGSHSLRYFSTAVSRGGRGPRYIAVEYVDDTQFLRPDSD 60  
  
Qy 61 AAPRMEPREPWEQEGPQYWEWTTGYAKANAQTDVVALNRLNRRYVNSAGSHTLQGMN 120  
Db 61 AAPRMEPREPWEQEGPQYWEWTTGYAKANAQTDVVALNRLNRRYVNSAGSHTLQGMN 120  
  
Qy 121 GCDMGPDGRLLRGHQYHAYDGKDYISLNEDLRGWTAAADTVAQITQRYEAEYAEPRTY 180  
Db 121 GCDMGPDGRLLRGHQYHAYDGKDYISLNEDLRGWTAAADTVAQITQRYEAEYAEPRTY 180  
  
Qy 181 LEGECLELLRRLYENGLLETQADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQR 240  
Db 181 LEGECLELLRRLYENGLLETQADPPKAAHVAHPISDHEATLRCWALGFYPAEITLTWQR 240  
  
Qy 241 DGEQEQDTBELVETPRAGDCTFKQAAVVPVSGEEQRYTCHVQHEGLPQLILRWESQP 300  
Db 241 DGEQEQDTBELVETPRAGDCTFKQAAVVPVSGEEQRYTCHVQHEGLPQLILRWESQP 300  
  
Qy 301 PTPPIGVIGVAGLVGLGAVVTGAVVAAVWWRKKSDDNRNGSYQAQVTDTSAGSGVSLTAN 360  
Db 301 PTPPIGVIGVAGLVGLGAVVTGAVVAAVWWRKKSDDNRNGSYQAQVTDTSAGSGVSLTAN 360  
  
Qy 361 KV 362  
Db 361 KV 362  
  
RESULT 7  
ADP23768  
ID ADP23768 standard; protein; 362 AA.

XX ADP23768;  
AC 18-NOV-2004 (first entry)  
DT XX  
XX PRO polypeptide SEQ ID NO:946.  
DE XX  
XX PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;  
KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;  
KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.  
XX  
XX Unidentified.  
XX  
XX WO2004041170-A2.  
XX  
XX 21-MAY-2004.  
XX  
XX 30-OCT-2003; 2003WO-US034312.  
XX  
XX 01-NOV-2002; 2002US-0423394P.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Clark H, Schoenfeld J, Van Lookeren M, Williams BM, Wood WI;  
PI Wu TD;  
XX  
XX WPI; 2004-419628/39.  
XX  
XX N-PSDB; ADP23767.  
XX  
XX New PRO polypeptides and polynucleotides, useful for treating e.g.  
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated  
PT renal disease, or demyelinating diseases of the central or peripheral  
PT nervous system.  
XX  
XX  
PS Claim 7; SEQ ID NO 946; 2940pp; English.  
XX  
XX The invention relates to a novel isolated nucleic acid and the PRO  
CC polypeptide encoded by it. A protein of the invention has  
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,  
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,  
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide  
CC of the invention may have a use in gene therapy. The PRO polypeptide, its  
CC agonist, antagonist, or antibody that specifically binds to the  
CC polypeptide is useful for treating an immune related disorder such as  
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
CC disease, a demyelinating disease of the central or peripheral nervous  
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,  
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary  
CC disease, infectious or autoimmune chronic active hepatitis, primary  
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's  
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin  
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic  
CC disease, asthma, allergic rhinitis, atopic dermatitis, food  
CC hypersensitivity, urticaria, an immunologic disease of the lung,  
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity  
CC pneumonitis, a transplantation associated disease, graft rejection or  
CC graft-versus-host disease. The present sequence represents a PRO protein  
CC of the invention.  
XX  
SQ Sequence 362 AA;  
  
Query Match 72.1%; Score 261; DB 8; Length 362;  
Best Local Similarity 99.7%; Pred. No. 1.4e-229;  
Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 MAPRSLLLLSGALALTDWAGSHSLRYFSTAVSRGGRGPRYIAVEYVDDTQFLRPDSD 60  
Db 1 MAPRSLLLLSGALALTDWAGSHSLRYFSTAVSRGGRGPRYIAVEYVDDTQFLRPDSD 60

QY 61 AAI PRMEPREPVEQEGPOYWEWTTGYAKANAQTDRLVALNLLRRYNQSEAGSHTLQGNW 120  
Db |||||  
FT 61 AAI PRMEPREPVEQEGPOYWEWTTGYAKANAQTDRLVALNLLRRYNQSEAGSHTLQGNW 120  
QY 121 GCDMPDGLRLRGYHQHAYDGDYISLNEDLSWTAADTVAGITQRFYEAEEYAEFFRY 180  
Db |||||  
FT 121 GCDMPDGLRLRGYHQHAYDGDYISLNEDLSWTAADTVAGITQRFYEAEEYAEFFRY 180  
QY 181 LECECLELRLRYLENGLETQRADPPKAVAHHPISDHEATLRCWALGFYPAEITLTWQR 240  
Db |||||  
FT 181 LECECLELRLRYLENGLETQRADPPKAVAHHPISDHEATLRCWALGFYPAEITLTWQR 240  
QY 241 DGEETQDTVELVETRPAGDGTQKWAADVVPSEGEQRYTCHVQHEGLPQPLILRWEQSPQ 300  
Db |||||  
FT 241 DGEETQDTVELVETRPAGDGTQKWAADVVPSEGEQRYTCHVQHEGLPQPLILRWEQSPQ 300  
QY 301 PTPIPIVIGIAGLVGLGAVVTGAVAAVMWRKSSDRNGSYSQAAVTDQAQSGVSLTAN 360  
Db |||||  
FT 301 PTPIPIVIGIAGLVGLGAVVTGAVAAVMWRKSSDRNGSYSQAAVTDQAQSGVSLTAN 360  
QY 361 KV 362  
Db ||  
FT 361 KV 362

RESULT 8  
ID ADS74309  
XX ADS74309 standard; protein; 362 AA.  
AC ADS74309;  
XX  
XX 16-DEC-2004 (first entry)  
XX PRO polypeptide PRO81414, role in immune-related disease.  
XX PRO81414; psoriasis; ulcerative colitis; gastrointestinal-gen.;  
KW antipsoriatic; gene therapy.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..17  
FT /label= Signal\_peptide  
FT Protein 18..362  
FT /label= Mature\_protein  
FT Region 22..200  
FT /note= "Class I histocompatibility antigen"  
FT Modified-site 107..110  
FT /note= "N-glycosylation site"  
FT Modified-site 118..123  
FT /note= "N-myristoylation site"  
FT Region 131..136  
FT /note= "Crystallins beta and gamma 'Greek key' motif signature"  
FT Modified-site 166..173  
FT /note= "Tyrosine kinase phosphorylation site"  
FT Domain 217..282  
FT /label= Immunoglobulin  
FT Region 278..284  
FT /note= "Immunoglobulins and major histocompatibility complex proteins signature"  
FT Domain 304..324  
FT /label= Transmembrane  
FT Modified-site 307..312  
FT /note= "N-myristoylation site"  
FT Modified-site 316..321  
FT /note= "N-myristoylation site"  
FT Modified-site 321..326  
FT /note= "N-myristoylation site"  
FT Modified-site 330..333  
FT /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"  
FT

FT Modified-site 331..334  
FT /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"  
FT Modified-site 352..357  
FT /note= "N-myristoylation site"  
FT Modified-site 354..359  
FT /note= "N-myristoylation site"  
FT Region 360..362  
FT /note= "Microbodies C-terminal targeting signal"  
XX WO2004081199-A2.  
PN  
XX 23-SEP-2004.  
PD  
XX 10-MAR-2004; 2004WO-US007862.  
PF  
XX 11-MAR-2003; 2003US-0454025P.  
PR (GETH ) GENENTECH INC.  
XX  
XX Baldwin D, Bodary S, Clark H, Fong S, Gurney AL, Williams PM;  
PI WPI: 2004-668955/65.  
XX N-PSDB; ADS74308.  
DR  
XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and treating psoriasis, Crohn's disease, Ulcerative Colitis, or rheumatoid arthritis.  
PT  
XX Claim 9; SEQ ID NO 28; 166pp; English.  
PS  
XX The present sequence is the protein sequence of novel human PRO polypeptide PRO81414. The invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to as PRO polypeptides that are useful in the diagnosis and treatment of immune-related diseases. Microarray analysis showed that expression of PRO81414 is up-regulated 1.2-fold in lesional skin as compared to non-lesional skin from psoriasis patients and up-regulated 1.5-fold in colon samples from ulcerative colitis patients as compared to normal colon. It is also down-regulated 2-fold upon differentiation of monocytes into macrophages after 7 days in differentiation media and up-regulated 4-fold in dendritic cells upon activation with LPS. PRO81414 can be used in a claimed method of identifying a compound that inhibits expression of the gene encoding it. The candidate compound is especially an antiseptic nucleic acid. The PRO polypeptide can be obtained by recombinant expression, especially in CHO, Escherichia coli or yeast host cells. The polypeptide, its antagonist or an antibody that binds the polypeptide are used in claimed methods for the alleviation or diagnosis of psoriasis and ulcerative colitis.  
XX  
SQ Sequence 362 AA;  
Query Match 72.1%; Score 261; DB 8; Length 362;  
Best Local Similarity 99.7%; Pred No. 1.4e-229;  
Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MAPRSLLLLSGALALTDWAGSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSD 60  
Db |||||  
FT 1 MAPRSLLLLSGALALTDWAGSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSD 60  
QY 61 AAI PRMEPREPVEQEGPOYWEWTTGYAKANAQTDRLVALNLLRRYNQSEAGSHTLQGNW 120  
Db |||||  
FT 61 AAI PRMEPREPVEQEGPOYWEWTTGYAKANAQTDRLVALNLLRRYNQSEAGSHTLQGNW 120  
QY 121 GCDMPDGLRLRGYHQHAYDGDYISLNEDLSWTAADTVAGITQRFYEAEEYAEFFRY 180  
Db |||||  
FT 121 GCDMPDGLRLRGYHQHAYDGDYISLNEDLSWTAADTVAGITQRFYEAEEYAEFFRY 180  
QY 181 LECECLELRLRYLENGLETQRADPPKAVAHHPISDHEATLRCWALGFYPAEITLTWQR 240  
Db |||||  
FT 181 LECECLELRLRYLENGLETQRADPPKAVAHHPISDHEATLRCWALGFYPAEITLTWQR 240  
QY 241 DGEETQDTVELVETRPAGDGTQKWAADVVPSEGEQRYTCHVQHEGLPQPLILRWEQSPQ 300

Db 241 DGEQTDTELVEVTRPAGDTGFKWAAVVPVSGEQYTCHVQHEGLPQPLILRWEQSPQ 300  
 Qy 301 PTPIVIGVAGLVVLGAVVTGAVVAAVMMRKSSDRNRGSYSQAAVTDSSAQSGVSLTAN 360  
 Db 301 PTPIVIGVAGLVVLGAVVTGAVVAAVMMRKSSDRNRGSYSQAAVTDSSAQSGVSLTAN 360  
 Qy 361 KV 362  
 Db 361 KV 362

RESULT 9  
 ADJ70081  
 ID ADJ70081 standard; protein; 442 AA.  
 AC ADJ70081;  
 XX  
 DT 06-MAY-2004 (first entry)  
 DE Human heat mitochondrial protein as a therapeutic target SeqID1887.  
 XX  
 KW mitochondrial; human; screening assay; diabetes mellitus;  
 KW Huntington's disease; osteoarthritis;  
 KW Leber's hereditary optic neuropathy; LHON;  
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;  
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;  
 KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;  
 KW osteopathic; ophthalmological; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003087768-A2.  
 XX  
 PD 23-OCT-2003.  
 XX  
 PF 04-APR-2003; 2003WO-US010870.  
 XX  
 PR 12-APR-2002; 2002US-0372843P.  
 PR 17-JUN-2002; 2002US-0389987P.  
 PR 20-SEP-2002; 2002US-0412418P.  
 XX  
 PA (MITO-) MITOKOR.  
 PA (BUCK-) BUCK INST AGE RES.  
 XX  
 PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;  
 PI Warnock DE;  
 XX  
 DR WPI; 2003-845369/78.  
 XX  
 PT Identifying a mitochondrial target for drug screening assays and for  
 PT treating diseases associated with altered mitochondrial function,  
 PT comprises detecting a modified polypeptide in a sample and correlating  
 PT with the disease.  
 XX  
 PS Claim 1; SEQ ID NO 1887; 180pp; English.  
 XX  
 CC This invention relates to novel mitochondrial targets that can be used  
 CC for therapeutic intervention in treating a disease associated with  
 CC altered mitochondrial function. Specifically, it refers to a method for  
 CC identifying proteins of the human heart mitochondrial proteome that are  
 CC useful for drug screening assays, as well as therapeutic targets. The  
 CC present invention describes a method for identifying such proteins that  
 CC can be used in the treatment of various diseases associated with altered  
 CC mitochondrial function including diabetes mellitus, Huntington's disease,  
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these  
 CC compositions have neuroprotective, nootropic, antidiabetic,  
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
 CC cytostatic activities. This polypeptide sequence is a human heart  
 CC mitochondrial protein of the invention.  
 XX

SQ Sequence 442 AA;  
 Query Match 67.4%; Score 244; DB 7; Length 442;  
 Best Local Similarity 99.7%; Pred. No. 5.7e-214;  
 Matches 344; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MAFRSLLLSGALALTDTWAGSHLSLRYSTAVSRGEGPRYIAVEYVDDTQFLRFDS 60  
 Db 1 MAFRSLLLSGALALTDTWAGSHLSLRYSTAVSRGEGPRYIAVEYVDDTQFLRFDS 60  
 Qy 61 AAI PRMEPREPWVEQEGPOYWEWTTGYAKANAOTDRVALNLLRRYNSAGSHTLQGMN 120  
 Db 61 AAI PRMEPREPWVEQEGPOYWEWTTGYAKANAOTDRVALNLLRRYNSAGSHTLQGMN 120  
 Qy 121 GCDMGPDGRLRGYHQHAYDGKDYISLNEDLRSWTAADTVAQITQRFYAEAEPEPTY 180  
 Db 121 GCDMGPDGRLRGYHQHAYDGKDYISLNEDLRSWTAADTVAQITQRFYAEAEPEPTY 180  
 Qy 181 LECECELELLRRYLENGLETQORADPPKAHVAAHPISDHEATLRCWALGFYPAITLTW 240  
 Db 181 LECECELELLRRYLENGLETQORADPPKAHVAAHPISDHEATLRCWALGFYPAITLTW 240  
 Qy 241 DGEEOQTDTELVEVTRPAGDTGFKWAAVVPVSGEQYTCHVQHEGLPQPLILRWEQSPQ 300  
 Db 241 DGEEOQTDTELVEVTRPAGDTGFKWAAVVPVSGEQYTCHVQHEGLPQPLILRWEQSPQ 300  
 Qy 301 PTPIVIGVAGLVVLGAVVTGAVVAAVMMRKSSDRNRGSYSQAA 345  
 Db 301 PTPIVIGVAGLVVLGAVVTGAVVAAVMMRKSSDRNRGSYSQAA 345

RESULT 10  
 AAB43986  
 ID AAB43986 standard; protein; 271 AA.  
 AC AAB43986;  
 XX  
 DT 08-FEB-2001 (first entry)  
 DE Human cancer associated protein sequence SEQ ID NO:1431.  
 XX  
 KW Human; cancer associated gene; cancer antigen; detection; cancer;  
 KW diagnosis; cytostatic; proliferative; vulnery; immunomodulator;  
 KW antidiabetic; antiaesthetic; antirheumatic; antithyroid; antiviral;  
 KW antiinflammatory; antihypertoid; antiallergic; antibacterial; cardiant;  
 KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;  
 KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;  
 KW immune disorder; haematopoietic cell disorder; autoimmune disorder;  
 KW allergic reaction; graft versus host disease; organ rejection;  
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
 KW neurological disease; drug screening.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200055350-A1.  
 XX  
 PD 21-SEP-2000.  
 XX  
 PF 08-MAR-2000; 2000WO-US005882.  
 XX  
 PR 12-MAR-1999; 99US-0124270P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Ruben SM;  
 XX  
 DR WPI; 2000-587533/55.  
 DR N-PSDB; AAC78195.  
 XX  
 PT Novel isolated nucleic acids comprising sequences encoding peptides  
 PT useful for treating or diagnosing e.g. cancer.  
 XX  
 PS Claim 11; Page 2115-2116; 2352pp; English.

XX AAC77607 to AAC78448 encode the human cancer associated proteins given in  
 CC AAB43398 to AAB44239. The proteins can have activities based on the  
 CC tissues and cells the genes are expressed in. Example of activities  
 CC include: cytostatic; proliferative; vulnerable; immunomodulator;  
 CC antidiabetic; antiaschmatic; antirheumatic; antibacterial; antiviral;  
 CC dermatological; neuroprotective; cardiac; thrombolytic; coagulant;  
 CC neotropic; vasotropic; antipsoriatic and antiangiogenic. The  
 CC polynucleotides and polypeptides can be used for preventing, treating or  
 CC ameliorating medical conditions and diagnosing pathological conditions.  
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
 CC the present invention may be used to treat immune disorders by activating  
 CC or inhibiting the proliferation, differentiation or mobilisation of  
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
 CC disorders, allergic reactions, graft versus host disease and organ  
 CC rejection, modulate haemostatic or thrombolytic activity, modulate  
 CC inflammation, cancer, cardiovascular disorders, neurological disease and  
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to  
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of  
 CC the present invention  
 XX  
 SQ Sequence 271 AA;

Query Match 54.1%; Score 196; DB 3; Length 271;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-170;  
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPRSLLLLSGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRFDSD 60  
 DB 7 MAPRSLLLLSGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRFDSD 66  
 QY 61 AAI PRMEPREPWVEQEGPYWETTTGYAKANAQTDRLVALNRLRRYNQSEAGSHTLQGMN 120  
 DB 67 AAI PRMEPREPWVEQEGPYWETTTGYAKANAQTDRLVALNRLRRYNQSEAGSHTLQGMN 126  
 QY 121 GCDMGPDGRLRGYHQHAYDGKDYISLNEDLSRWTAAADTVAQITQRFYEAEYAEFEFTY 180  
 DB 127 GCDMGPDGRLRGYHQHAYDGKDYISLNEDLSRWTAAADTVAQITQRFYEAEYAEFEFTY 186  
 QY 181 LEGECLELLRRYLENG 196  
 DB 187 LEGECLELLRRYLENG 202

RESULT 11  
 ABG26726  
 ID ABG26726 standard; protein; 677 AA.  
 XX AC ABG26726;  
 XX  
 DT 18-FEB-2002 (first entry)  
 DE Novel human diagnostic protein #26717.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.  
 XX Homo sapiens.  
 XX WO200175067-A2.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US008631.  
 XX  
 PR 31-MAR-2000; 2000US-00540217.  
 PR 23-AUG-2000; 2000US-00649167.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.  
 DR N-PSDB; AAS90913.  
 XX  
 PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX  
 PS Claim 20; SEQ ID NO 57085; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic  
 CC amino acid sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 677 AA;

Query Match 54.1%; Score 196; DB 4; Length 677;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-170;  
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPRSLLLLSGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRFDSD 60  
 DB 310 MAPRSLLLLSGALALTDTWAGSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRFDSD 369  
 QY 61 AAI PRMEPREPWVEQEGPYWETTTGYAKANAQTDRLVALNRLRRYNQSEAGSHTLQGMN 120  
 DB 370 AAI PRMEPREPWVEQEGPYWETTTGYAKANAQTDRLVALNRLRRYNQSEAGSHTLQGMN 429  
 QY 121 GCDMGPDGRLRGYHQHAYDGKDYISLNEDLSRWTAAADTVAQITQRFYEAEYAEFEFTY 180  
 DB 430 GCDMGPDGRLRGYHQHAYDGKDYISLNEDLSRWTAAADTVAQITQRFYEAEYAEFEFTY 489  
 QY 181 LEGECLELLRRYLENG 196  
 DB 490 LEGECLELLRRYLENG 505

RESULT 12  
 AAG64618  
 ID AAG64618 standard; protein; 274 AA.  
 XX AC AAG64618;  
 XX  
 DT 12-SEP-2001 (first entry)  
 DE Human cancer cell specific HLA-F antigen SEQ ID 5.  
 XX  
 KW HLA-F antigen; cancer cell specific; human.  
 XX Homo sapiens.  
 XX JP2001095584-A.  
 XX  
 PD 10-APR-2001.

XX 30-SEP-1999; 99JP-00279566.  
 XX 30-SEP-1999; 99JP-00279566.  
 XX (EGAW/) EGAWA K.  
 PA (MEDI-) MEDINET KK.  
 PA (KIMU/) KIMURA K.  
 XX WPI; 2001-360493/38.  
 DR N-PSDB; AAH45556.  
 XX Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.  
 PT Claim 2; Page 10-11; 12pp; Japanese.  
 XX This invention relates to a cancer cell specific HLA-F antigen. The  
 CC invention includes DNA encoding the antigen, and a method for the  
 CC preparation of the cancer cell specific HLA-F antigen. The antigen may be  
 CC used in a method to diagnose cancer, in which the protein is used to  
 CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present  
 CC sequence represents the cancer cell-specific HLA-F antigen of the  
 CC invention  
 XX SQ Sequence 274 AA;  
 Query Match 48.3%; Score 175; DB 4; Length 274;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-151;  
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 22 GSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPREPWEQGPQYW 81  
 DB 1 GSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPREPWEQGPQYW 60  
 QY 82 EWTGTGAKANAQTDRLVALNRLRRYNOSEAGSHTLQGMNGCDMPDGRLLRGYHAYDG 141  
 DB 61 EWTGTGAKANAQTDRLVALNRLRRYNOSEAGSHTLQGMNGCDMPDGRLLRGYHAYDG 120  
 QY 142 KOYISLNEDLRSWTAADTVAQITQRFYEAEYAEFEFTYLEGECLELLRRYLENG 196  
 DB 121 KOYISLNEDLRSWTAADTVAQITQRFYEAEYAEFEFTYLEGECLELLRRYLENG 175  
 RESULT 13  
 ADF55588  
 ID ADF55588 standard; protein; 274 AA.  
 XX ADF55588;  
 AC ADF55588;  
 DT 12-FEB-2004 (first entry)  
 XX Fragment #1 of human cancer-cell specific HLA-F antigen.  
 DE Cancer; human leukocyte antigen-F; HLA-F;  
 KW Cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
 KW major histocompatibility complex; MHC; cancer cell; human.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX JP2003012544-A.  
 PN 15-JAN-2003.  
 PD 27-MAR-2002; 2002JP-00088991.  
 PF 27-MAR-2001; 2001JP-00090121.  
 XX (EGAW/) EGAWA K.  
 PA (MEDI-) MEDINET KK.  
 PA (KIMU/) KIMURA Y.  
 XX WPI; 2003-486263/46.  
 DR N-PSDB; ADF55585.

XX Agent for preventing and treating cancer, comprising human leukocyte  
 PT antigen-F DNA, or a plasmid or viral vector comprising the DNA.  
 XX Claim 7; SEQ ID NO 5; 19pp; Japanese.  
 XX The present invention relates to an agent for preventing or treating  
 CC cancer. The agent comprises a portion or a complete sequence of a human  
 CC leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of  
 CC presenting a cancer-cell specific antigen transformed with HLA-F DNA, or  
 CC a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte  
 CC (CTL) inducer which induces CTL which is non-specific to an organ, is  
 CC unrestricted to the major histocompatibility complex (MHC) and specific  
 CC to a cancer cell, and an anti-HLA-F antibody. The agent of the invention  
 CC is useful for treating or preventing cancer. A cell capable of presenting  
 CC a cancer-cell specific antigen is useful for measuring HLA-F antigen and  
 CC for diagnosing cancer. The present sequence represents part of the human  
 CC cancer-cell specific HLA-F antigen.  
 XX SQ Sequence 274 AA;  
 Query Match 48.3%; Score 175; DB 7; Length 274;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-151;  
 Matches 175; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 22 GSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPREPWEQGPQYW 81  
 DB 1 GSHSLRYFSTAVSRPGRGEPRIYAVEYVDDTQFLRFDSDAAIPRMEPREPWEQGPQYW 60  
 QY 82 EWTGTGAKANAQTDRLVALNRLRRYNOSEAGSHTLQGMNGCDMPDGRLLRGYHAYDG 141  
 DB 61 EWTGTGAKANAQTDRLVALNRLRRYNOSEAGSHTLQGMNGCDMPDGRLLRGYHAYDG 120  
 QY 142 KOYISLNEDLRSWTAADTVAQITQRFYEAEYAEFEFTYLEGECLELLRRYLENG 196  
 DB 121 KOYISLNEDLRSWTAADTVAQITQRFYEAEYAEFEFTYLEGECLELLRRYLENG 175  
 RESULT 14  
 AAG64619  
 ID AAG64619 standard; protein; 215 AA.  
 XX AAG64619;  
 AC AAG64619;  
 DT 12-SEP-2001 (first entry)  
 XX Human cancer cell specific HLA-F antigen SEQ ID 6.  
 DE HLA-F antigen; cancer cell specific; human.  
 KW HLA-F antigen; cancer cell specific; human.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX JP2001095584-A.  
 PN 10-APR-2001.  
 PD 30-SEP-1999; 99JP-00279566.  
 PF 30-SEP-1999; 99JP-00279566.  
 PR 30-SEP-1999; 99JP-00279566.  
 XX (EGAW/) EGAWA K.  
 PA (MEDI-) MEDINET KK.  
 PA (KIMU/) KIMURA K.  
 XX WPI; 2001-360493/38.  
 DR N-PSDB; AAH45557.  
 XX Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.  
 PT Claim 1; Page 11-12; 12pp; Japanese.  
 XX This invention relates to a cancer cell specific HLA-F antigen. The  
 CC invention includes DNA encoding the antigen, and a method for the

CC preparation of the cancer cell specific HLA-F antigen. The antigen may be  
CC used in a method to diagnose cancer, in which the protein is used to  
CC detect anti-HLA-F antibodies in bodily fluids of the patient. The present  
CC sequence represents the cancer cell-specific HLA-F antigen of the  
CC invention

XX SQ Sequence 215 AA;  
Query Match 42.3%; Score 153; DB 4; Length 215;  
Best Local Similarity 100.0%; Pred. No. 3.9e-131; Indels 0; Gaps 0;  
Matches 153; Conservative 0; Mismatches 0;  
QY 44 IAVEYVDDTQFLRFSDAAIPRMEPREPWVEQGPQYWEWTTGYAKANAQTDRVALRNLL 103  
Db 1 IAVEYVDDTQFLRFSDAAIPRMEPREPWVEQGPQYWEWTTGYAKANAQTDRVALRNLL 60  
QY 104 RRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQAHDGKDYISLNEDLSWTAADTVAQI 163  
Db 61 RRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQAHDGKDYISLNEDLSWTAADTVAQI 120  
QY 164 TORFYEAEEYAEFFTYLGECELELLRRYLENG 196  
Db 121 TORFYEAEEYAEFFTYLGECELELLRRYLENG 153

RESULT 15  
ADP55589  
ID ADP55589 standard; protein; 215 AA.  
XX AC ADP55589;  
XX DT 12-FEB-2004 (first entry)  
XX DE Fragment #2 of human cancer-cell specific HLA-F antigen.  
XX KW Cancer; human leukocyte antigen-F; HLA-F;  
XX KW cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;  
XX KW major histocompatibility complex; MHC; cancer cell; human.  
XX OS Homo sapiens.  
XX PN JP2003012544-A.  
XX PD 15-JAN-2003.  
XX PF 27-MAR-2002; 2002JP-00088991.  
XX PR 27-MAR-2001; 2001JP-00090121.  
XX PA (EGAW/) EGAWA K.  
XX PA (MEDI-) MEDINET KK.  
XX PA (KIMU/) KIMURA Y.  
XX DR WPI; 2003-486263/46.  
XX DR N-PSDB; ADP55586.  
XX PT Agent for preventing and treating cancer, comprising human leukocyte  
XX PT antigen-F DNA, or a plasmid or viral vector comprising the DNA.  
XX PS Claim 7; SEQ ID NO 6; 19pp; Japanese.  
XX CC The present invention relates to an agent for preventing or treating  
XX CC cancer. The agent comprises a portion or a complete sequence of a human  
XX CC leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of  
XX CC presenting a cancer-cell specific antigen transformed with HLA-F DNA, or  
XX CC a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte  
XX CC (CTL) inducer which induces CTL which is non-specific to an organ, is  
XX CC unrestricted to the major histocompatibility complex (MHC) and specific  
XX CC to a cancer cell, and an anti-HLA-F antibody. The agent of the invention  
XX CC is useful for treating or preventing cancer. A cell capable of presenting  
XX CC a cancer-cell specific antigen is useful for measuring HLA-F antigen and  
XX CC for diagnosing cancer. The present sequence represents part of the human  
XX CC cancer-cell specific HLA-F antigen.

XX SQ Sequence 215 AA;  
Query Match 42.3%; Score 153; DB 7; Length 215;  
Best Local Similarity 100.0%; Pred. No. 3.9e-131; Indels 0; Gaps 0;  
Matches 153; Conservative 0; Mismatches 0;  
QY 44 IAVEYVDDTQFLRFSDAAIPRMEPREPWVEQGPQYWEWTTGYAKANAQTDRVALRNLL 103  
Db 1 IAVEYVDDTQFLRFSDAAIPRMEPREPWVEQGPQYWEWTTGYAKANAQTDRVALRNLL 60  
QY 104 RRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQAHDGKDYISLNEDLSWTAADTVAQI 163  
Db 61 RRYNQSEAGSHTLQGMNGCDMPDGRLLRGYHQAHDGKDYISLNEDLSWTAADTVAQI 120  
QY 164 TORFYEAEEYAEFFTYLGECELELLRRYLENG 196  
Db 121 TORFYEAEEYAEFFTYLGECELELLRRYLENG 153  
Search completed: July 13, 2005, 09:14:41  
Job time : 168 secs